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09/846,456 11/2/03

From:

Leffers, Gerald

Sent:

Thursday, May 01, 2003 3:12 PM STIC-Biotech/ChemLib

To: Subject:

STIC-Biotech/Chem FW: 09/846,456

Thanks for your help, gerry leffers

Gordd G. Leffors Tr., PhD Examiner, Art Unit 1636 Crystal Mall 1, Room 11A09 703-308-6232

-----Original Message-----

From:

Fredman, Jeffrey

Sent:

Thursday, May 01, 2003 2:47 PM

T : Subject: Leffers, Gerald RE: 09/846,456

Gerald,

I don't think you need approval unless it is a rush. You are under the 10,000 nucleotide limit.

Jeff

----Original Message----

From:

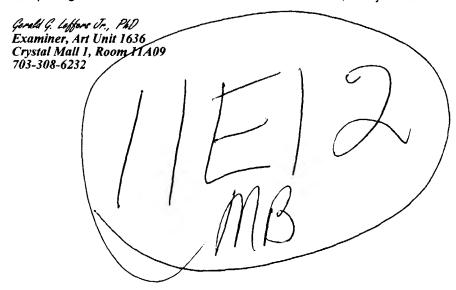
Leffers, Gerald

Sent:

Thursday, May 01, 2003 2:00 PM

To: Subject: Fredman, Jeffrey 09/846,456

Hi Jeff, please approve the following searches for this application. Total nucleic acid length is ~7 kb. SEQ ID NO: 1 (3.2kb), SEQ ID NO: 2 (357 nts), SEQ ID NO: 3 (2.8 kb), SEQ ID NO: 5 (159 nts). Claims drawn to 30 contiguous nucleotides of SEQ ID NOS: 3 & 5; 300 contiguous nucleotides of SEQ ID NO: 1. Other claims to nucleic acids comprising all of SEQ ID NO: 1 or SEQ ID NO: 2. Thanks, Gerry Leffers



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May 9, 2003, 11:17:01 ; Search time 3647.97 seconds (without alsahments) 9746.207 Million cert spdares/sec 1975 Transport Colorado action (53) 41092HD 2054640 seqs, 14551402878 residues Total number of hits satisfying chosen parameters: l acagggcatggtggcaggtg..... FOST processing: Minimum Match 6%
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28339 28519 27799 27919 27979 28159 28399 27619 27859 28099 28219 28279 28459 27739 28579 1730 1785 27679 1845 1903 1963 2023 2083 2203 2263 2323 2383 2443 2503 2563 2623 2683 27980 TTAAAAGGGGGCIGGTCCAFALTCITCTGTGTTTGTTTGTTTGTTTGTTTTTTTNNNNNNN AGGAGACCTTGTGGCCTCCACGTGCACTTCCAGGGCCTGCTTGGGCCTCTTCTACGGGTC TGTCCTGAGTCTTCTATGAA-- -- TCCTTCAGGCCAGATTCATATTAGACTCTTCACA TTAAATATITAGAC -ATGCIGICTAGGCCTGCATTCCTACTCTTGCCTTTTTTTGCC CCTCCAGTGTTTTGGCGTAGTTTTGCTCCCCTACAGCCAAAGGCAAACAGAGAAGTTGGAG 1964 GTCTGGAGTGGCTACAJAATTTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGT 27860 GTCTGGAGTGGCTACATATTTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGT ATACAAACTAAATACAAGTCCTGTGTTTTTTTTTCACAGGGGGCTGATCAATATAATGAAA TATCAAAAATCAAAGTCCAGGTTTG1GGGGGAAAACAAAAGCAGCCCATTACCCAGAGG ACTGTCCGGCT TOPPCTCACCCAGCCTAGGGCTTTGAAAGGGAAACAAAGACAAGACAA ATTCCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCG AGCCCAGCGCT1CCCGCGCGTCT1AGGCCGGCGGGCCCGGGCGGGGGGGAAGGGGACGCAGA CCGCGGACCCTAAGACACTGCTGTACCCTCCACCCCCACCCCACCCCACCTCCCC 2564 2324 2384 2504 2624 1846 28046 2264 28220 28280 28460 28520 1671 1731 1786 1904 2024 2144 28160 28400 27680 3 9 å 3 ਤ ò q ŝ ú q a ć 3 ŝ 5 ô a ं a ò £ ŝ ü á 5 ô ŝ ć ŝ ŝ ć ડે ò ò

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On Jan 15, 2002 this sequence version replaced glightable.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping cloue ranne. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submission only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear PRI 11-JAN-2002
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Human DNA sequence from clone RPI1-21787 on chromosome 9, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemistry or covered by high quality data (i.e., pired quality) 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least, one plasmid subclone or more than one M13 s.bclone; and the assembly was confirmed by restriction digest. The following
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Ebikaryota, Metazoa, Chordata: Craniala: Veriebraia: Euteleosiomi:
Mammalia: Eutheria: Primates: Catarrhin: Heminidae: Home.
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Cambridgeshire, CB10 1SA, UK. E-mail enquir.es:
humquery@sanger.ac.uk Clone requests: clone?equestcsanger.ac.uk
                           28760 ATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAATTGCGAGGGAGAGTGASTGGGSCCGG 28819
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2924 GACCCCCAGAGCCGAGCCGACCCITCTCTCCCGGGCTGCGGCAGGCCAGGGCAGGCAGC
                                                                                                                  2744 CTCCACGTGCTTTCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGGAAGGGGGCGGG
                                                                                                                                                                                                                                     2894 GAGGAGGGAGACACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCT
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Skuce, C.
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AL359182/c
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AUTHORS
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abbreviations are used to associate primary accession numbers given in the teature table with their source databases: En:, EMBL; Sw:, SWISSPECT; Tr:, TREMBL, WP. WORMPEP: Information on the WORMPEP database can be found at http://www.sanqer.ac.uk/Projects/C_legans/wormpep This sequence chromosome 9, constructed by the Sanger Centre Chromosome 5 Mapping Group. Further information can be found at http://www.sanqer.ac.uk/MGP/Cht9 RPII-217H7 is from the library RPCI-III constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                     'n
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                                                                                                                                                                                                          RPII-21787 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived from a single pUC clone. Restriction digest data confirm the assembly."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noie-"Sequence from reads from a short insert library derived from a single pUC clone. Restriction digest data
                                                                                                                                                                                                                                                                                            IMPORTANI: This sequence is not the entire insert of clone RP11-21787 it may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true right end of clone RP11-21787 is at 9617 in this sequence. The true left end of clone RP11-122F10 is at 72980 in this sequence. The true right end of clone RP11-122F10 is at 2000 this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2015) CCGGGGTGGCGGCGGGTGCCTGTAATCTCAGCTACTCGGGAGGTGGAGGTTGAATGAG 20092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AC026643), Assembly confirmed by restriction digest." 92050. 92163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- Sequence from reads from a short insert library
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/note-"Sequence from overlapping clone RPI1-122FIG
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VEGIOR: pBACe3.6
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98.8%; Pred. No. 0;
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/organism-"Homo sapiens
/db_xret-"taxon:9606"
/chromosome-"9"
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AGATGAAGAACAGGCCGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGCGAGGC 	TGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATAACATGCCAAAA FFILLITITTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	CCTGTCTCTACAAAAAAAAAAAAAAAAAAAAAAAAAAAA	CCAGCTACTTGGGAGGTAAGGTGGGAAGAACGCTTGAGGCCAGGGAGGTGAAGTGTACACTTTTTTTT	TGAGCCATGATGGATCACTGCACTCCAGCTGGTAGACAGAGAAGAAGACTGTCAA 	ARABARGABATGABABGAGAAAGAAAGGAGAGAGGAGGAGGAGGAGTGA3 	GOGAGGAGGGGGGGGGGAGGAAGGAAGGAAGGAAGAAAAAA	AAAAAACAAGATGAAACAGAGGGGGGGGGTTTTACGTAAATTGGTGGTGATGTGGTTTTTTTT	CAAGITITGACCCCAAAACCCAATITTATTGACCAAGGTTATTGITTGTTTGACTGAGGGAAGGGGAGGTTATTGAGTGACTGAC	AAAGCTCAT 11111111 AAAGCTCAT	COTTRETTINITIES TO CONSTRUCT OF THE CONTRACT CONTRACT OF THE C	GGGATGATCTCGACTCACTGTAACCTCTGCCCGGGGTTCAAGCGATTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT		TTCGAACTCCT [] []          TTCGAACTCCT	CACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGGGCACGGCTGGGCCGGCTGAGTCCTLTTTTTTTTTT	CATCCCTTTCTAAGGGAAACAGTCCATGGTGAAAGGGGGGGTGCGAGGGGGGGTTATG *** THEFT HITTELLE HITTELLE HITTELLE HITTELLE HITTELLE GATCCCTTTCTAAGGGCAAACAGCATGGTGGAAAGGGCCATGGGTGCAAAGGGCCATGGTGCAAGGGCCATGCCAGGTTATG	AGTACCTGGGACTCCAGAATTCCTTGCCTG	TCCTGAGTGTTGAT/                     TCCTGAGTGTTGAT/	GCTTGAGGCGTGGCCTGGAGATCCTGTTGACTGTAGGATGGAGGGAG
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18172 17881 18592 18352 18001 17941 17701 1551 1611 1671 1731 1787 18292 1965 2025 2085 2145 2205 2265 2325 2385 2445 2505 1905 1788 TIGACCICAGTTITGCCCAGAAIAAGGIGACATITAGTTIGTIGGCTIGATGGAIGACTI 1847 TCCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCGCAGCCCCGAG 2565 18051 AAAAGGGGCTGCTCCATATTGTTCTGTGTTTTTG------TTTGTTTGTTTGTTTTT 1612 GAAGAGTCTAAATGTGAATGTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTA **ACAAACTAAATACAAGTCCTGTGTTTTTATCACAGGGAGGCTGATCAATÅTAATGAAATT** 2206 GGGTCCTCTGAGGGACCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTTGCCTA TGTCCCCCTTCCCCTCACCCCAGCCTAGGCCTTTGAAAGGAAACAAAAGACAAAAA GCTGAGGAAACTAACAAAGGAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAAT AAATATTIAGAG - - ATGGIGTGFAGGCCTGCATTCCTACCTTTTTTTTTTGCCCC 1552 GTAGGCTTGGGGCAGCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGT GGAGACCTTGTGGCCTCCACGTGCACTTCCAGGCCCTGCTTGGGCCTCTTCTACGGGTCT 1732 GTCCTGAGTCTTCTATGAAT ---- CCTTCAGGGCAGATTCATATTTAGACTCTTCACAGT CTGGAGTGGCTACATAATTTTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTAT TCAAAAATCAAAGTCCAGGTTTGTGGGGGAAAACAAAAGCAGCCCATTACCCAGAGGAC ATGTCTGCATGCAGGTGGGAGTTCTGGAATATGATGAGGAGCTGGAGGTGGGAAGAGAA TCCAGTGTTTTGGGTAGTTTTGCTCCCCTACAGCCAAAGGCAAACAGAGAGTTGGAGGT 1672 1848 1906 1966 2026 2086 2266 2326 2386 2446 2506 17700 1492 qa a q g qq g d 5 ğ 5 5 g 5 ò 셤 δý 5 ò ò a ò ò ò ô ò g ò ò qq ŝ õ ŝ ò ें ć ŝ

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201144 bp DNA LIBERT 194-APR-2001 and Sapiens ATP-binding cassette 1 sub-tamily A member 1 (ABCA1) AF287262
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Mammalia, Eutheria, Primates, Catarrinni, Hominidae, Homo.
1 (bases 1 to 201144)
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17640 TCCACTGGTGCCCTTGGCTGCCGGGAACGTGGACTAGAGAGTCTGGGGGCGAGGCCCGAG 17581
                                                                                                                                                          2746 CCACGIGCTTICIGCIGAGIGACIGAACIACATAAACAGAGGCCGGGAAAGAGGCCGGGAAAGAGAGGCCGGGA 2805
                                                                                                                                                                                                       2806 GGAGGGAGAGGACAGGCTTTGACCGATAGTAACCTCTGGGCTGGGTGCAGTCTAT 2865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2566 OCCASCICETECCGGGGGTCTTAGGCCGGGGGCCCGGGGGGGGGGAAGUGGAGACC
                                   (bases 1 to 201144)
n.Y., Cavelier.L., Chin.S., Rubin.E. and Chem. L.
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Direct Submission
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GGNGTEEDAFFYDNSTTPPYCNDIMKNLESSPLSRIIMKALKPILLVGKILYTPDTPAT
Submitted (13-JUL 2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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33931. 181457
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Matches 3077; Conservative
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Eukaryota: Metazoa; Chordata: Craniata; Vericebiata: Filte.Costomi
Mammalia; Eutheria; Primates: Patarrinn; Bennisae, Bomo.
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Preworly, Duverger, N., Mendery, A. and Santabarrou Fordy, S.,
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Patent: WO 0183746-A.3 (8-MAY 2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
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Santamarina-Fojo.s., Peterson.K.M., Knapper,C.L., Freeman,L.A.,
Remal.ey.A.T., Yang,X.-P., Haudenschild,C.C., Blackmon.E.E.,
Francois,T.L. and Brewer,H.B. Jr.
                           2581 GCGTCTTAGGCCGGCCCGGGCCGGGGGAAGGGGACGCAGACCGCGGACCCTAAGACA 2640
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                                                                                                                                                                                                        Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
                                                                                     2341 CACCCCAGCCTAGGCCTTTGAAAGGAAACAAAAGACAAGACAAAATGATTGGCGTCCTGA
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6615 .6877
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Regulation with binding cassette transporter
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AX060894 1643 bp DNA linear FAT 22-JAN-200"  AX060894 AX060894 1 G1:12406271  AX060894 1 G1:12406271  Human  Human	OBEST MATCH  46.0%; Score 1485.4; DB 6: Length 1643; Best Local Similarity 98.1%; Pred. No. 0; Matches 1615: Conservative 0; Mismatches 6: Lidels 26: Gaps 10; Matches 1615: Conservative 0; Mismatches 6: Lidels 26: Gaps 10; Matches 1615: Conservative 0; Mismatches 5: Lidels 26: Gaps 10; Matches 1615: Conservative 0; Mismatches 6: Lidels 26: Gaps 10; Matches 1615: Conservative 0; Mismatches 6: Lidels 26: Gaps 10; Matches 1616: Mismatches 6: Conservation 11; Matches 1616: Mismatches 6: Conservation 11; Matches 1616: Mismatches 6: Conservation 11; Matches 1616: Mismatches 6: Mismatches 1616: Mismatches 1616; Matches 1616: Mismatches 1616: Mismatches 1616; Mismatches 1616; Misma	THE HELLICATE THE THE THE TERM CONTROL OF THE	CCTACTCTGCCTTTTTTTTTTCCCCCTCCAGINTTTCGGTAGTTTTGCT-CCCCTACAG  [14] [14] [14] [14] [14] [14] [14] [14]
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VERSION KEYWORDS SOURCE

REFERENCE

AUTHORS

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E. (bases I to 175064)

KS Birren, B., Linton, L., Nusbaum, C., Lander, E., Alten, N., Anderson, M., Birren, B., Linton, L., Nusbaum, C., Lander, E., Alten, N., Anderson, M., Birren, B., Linton, L., Nolangelo, M., Collins, S., Collymore, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Bornico, L., Doyle, M., Ferreira, P., Firzhugh, W., Forres, C., Funke, R., Gage, D., Doyle, M., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaffird, A., Horton, L., Howland, J.C., Johnson, R., Macdonald, P., Mardas, A., Horton, L., Howland, J.C., Johnson, R., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McGurk, A., McKernan, K., McLaughlin, J., Melaris, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., C'Sonnell, F., Peterson, K., Pollara, V., Kiley, R., Koy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassilicy, H., Vo, A., Wheeler, J., Zimmer, A., and Zody, M., Wheeler, J., Submitted (21-007-1999) Whitehead Estitute/Wiff Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 22, 2000 this sequence version replaced qi:6454033.

All repeats were identified using RepeatMasker: html
Hip://ttp-genome-washington.edu/RM/RepeatMasker:html
                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleosioni,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 175064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Geneme Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M1: M77815; 100% of reads Sequencing vector: M1: M77815; 100% of reads Assembly program: Phrap: version 0.966731 (Consensus quality: 117571 bases at leas: 04) Consensus quality: 117574 bases at leas: 04) Consensus quality: 169440 bases at leas: 020 consensus quality: 169440 bases at leas: 020 linear size: 185000; agarose : 19 linear size: 185000; agarose : 19 linear size: 171264; sum-of cont.as quality coverage: 2.9 in Q20 bases; sus-of-contique outlity coverage: 3.2 in Q20 bases; sus-of-contique
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Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions?genome.wi.mit.edu
Center project Information
Center project name: L2510
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contig of 1707 bp in length
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Homo sapiens.
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Db 2966 AGATGTTCCTCTCGGGTCCTCTGAGGGACCTGGGGAGCTGGGAATCTCCAAGGC 3025	Oy 2253 AGTAGGTCGCCTATCAAAATCAAAGGTTCGGGTTGTGGGGGGAAAACAAAAGCAGCCCA 2312	Qy 2313 TTACCCAGAGACTGCCGCTTCCCCTCCAGCCTAGGCCTTGAAAGGAAACAAA 2372	320	Cy 2433 ATCCTCCGGCTGAGGAAACTAACAAAGGAAAAAAATTGCGGAAAGCAGGTTT 2492 	Qy       2493 AGAGAAGCAAATTCCACTGGTGCCCTTGGCTGCGGGAACTGGACTAGAGAGCTGGG 2552         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 2553 GCGCAGCCCCGAGCCCTTCCCGCGCGTCTTAGGCCGGCGCGCGC	Oy 2613 GGGGACGCAGACCCTAAGACCTGCTGTACCTCCACCCCACCCA	Qy 2673 CCCACCTCCCCCAACTCCCTAGATGTGTGGGGGGGGTGAACGTCGCCGTTTAAGGG 2732 	Oy 2733 GCGGGCCCCGGCTTCCTGCTGAGTGACTGAACTACATAAACAGAGGCCGGG 2792 	Oy 2793 AAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	OY 2853 CAGCCGAAICTATAAAAGGAACTAGTCCCGGAAAAACCCCGTAATTGCGAGCGA	е -	Qy 2973 GGGGGGGGCGCACCAACAGGGGGGTTCTCAGGGCGCTTTGCTCTTTTTT 3032	3 CCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAGAGACG 309	Qy 3093 CAAACACAAAAGTGGAAAACAGGTAAGAGCTCTCCAGTGACTTACTT	QY 3153 TTIGITTCGAGGCCAAGGAGGCTTCGGGAAGTGCTCGGGGACTTTGATCCGGAG 3212 	Gy 3213 CCCCACATCCCCACCTT 3231	RESOLT 10 AP25862351
/note-"assembly_fragment"	ı ou		misc_feature 9787, 12253 /note=massembly_fraqmint. misc_toature 12354, 15228 /note=assembly_fragment	ນ ຍ	n n (		74479 194297 /note-"assembly_tragment" 34400 38318 /note-"assembly_tragment"	mist_lecture 5041942639 mist_leature 4293645448 //note=assembly_fragment	ט ט נ	misc_lecture 55/195952 misc_lecture 5669359635 misc_feature 5669359635 misc_feature 5669359635	misc.reduire 39750. 303001 misc_teature 6376268437 misc_teature 6453# 7145# 7145#		Query Match 38.0%; Score 1227.8; DB 2; Length 175064; Best Local Similarity 98.7%; Pred. No. 0; Matches 1263; Conservative 0; Mismatches 2; Indeis 14; Gaps 2;	TIGAGTGGCTACATATTITACAUGACTGCAATTERVTGSCTGCAC 2012 HILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 2013 TTCACAAATGTATACAAACTAAATACAAGTCCTGT3TTTTATCACAGGSAGGTGGTCA 2572 	<pre>Qy 2073 ATAFAATGAAATTAAAAGGGGCTGGTCCATATTGTTCGTTTTTGTTTTTTTT</pre>	GCAGIA   -:   GCAGIA	Oy 2193 AGAIGTICCICTCGGGGTCCTGAGGACCTGGGAGCTCAGGCTGGGAATCTCGAAGGC 2252

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(c) Pullinger, C.R., Hakamata, H., Duchareau, P.N., Erd. C., Aduraceat, B.E., Fielding, C.J. and Kane, J.P.

Aduraceat, B.E., Fielding, C.J. and Kane, J.P.

Analysis of hABCl gene 5 end: additional peptide sequence, promoter region, and four polymorphisms

E. pomoter region, and four polymorphisms

E. pomoter region, and four polymorphisms

E. pomoter region, and four polymorphisms

E. phillinger, C.R., Hakamata, H., Duchateau, P.N., Eng. C., Direct Submission

N. Direct Submission

N. Submitted (20-APR-2000) Cardiovascular Research institute, Direct Submission

Franctisco, CA 94143 0130, USA

3 (bases 1 to 1167)

Avaiverat, B.E., Fielding, C.J., and Kane, J.P., Eng. C., Avaiverat, B.E., Fielding, C.J., and Kane, J.P., Eng. C., Avaiverat, B.E., Fielding, C.J., and Kane, J.P., Eng. C., Avaiverat, B.E., Fielding, C.J., and Kane, J.P., Eng. C., Submission
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1167 bp DNA Linear FRI 23-JUN-2000 Homo sapiens ATP binding cassette transporter 1 (ARCA1) gene, AF258623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-JUN-2000) Cardiovascular Research Institute.
University of California, San Francisco, 565 Parnassus Avenue, San
Francisco, CA 94143-0130. USA
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on Jun 23, 2000 this sequence version replaced q::7759713
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transporter-1, 5'UTR and promoter region.
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/db_xref*"taxon:9606*
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Saliren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Saliren, B., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boaldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Burkett, G., Casle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Hadora, J., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McIdrim, J., Moneus, L., Mortow, J., Naylor, J., Norman, C.H., U'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K.,
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Firren, H., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome, clone RPII-INIO
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27576: contiq of 855 bp
27676: gap of 100 bp
28532: contig of 856 bp
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45724: contig of 872 bp
45824: gap of 100 bp
46643: contig of 819 bp
                                                                                               contig of 844 bp
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22832: contig of 867 bp
22932: gap of 100 bp
23780: contig of 848 bp
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contig of 851 bp
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Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, E., Kothman, D., Stoyanos, R., Sancas, P., Spencer, B., Stange-Thömann, N., Stojanovic, N., Subramanian, A., Talamas, J., Iesłaye, S., Theodore, J., Triteli, A., Vassii, W., W., Talamas, J., Iesłaye, S., Theodore, J., Triteli, A., Vassii, W., Wiel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission Cody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission Cody, M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Chingert, J. Codo, M., Canter, Cambridge, M., Viel, R., Wyman, D., Ye, W.J., Change, Charles Street, Cambridge, M., Viel, I., Vasan, Canton, Caron, C., Canton, C., Canto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling as useful to identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequence to completion. In the event that the record is updated, the accession comber will in
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seg.wl.mit.edu
Contact: sequence_seubminssions?genome.wl.mit.edu
Contact: Sequence_status
Center project name: L2512
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2804: contig of 870 bp in :enath:
gap of 100 bp in :enath:
3745: contig of 841 bp in length
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contra of 859 tp in length
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18042 18141: gap of 1669 hp

18042 19009: contiq of 868 hp

19000 19109: gap of 1808 hp i
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11322: contiq of 845 5p
22: gap of 100 bp
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12302: contig of 886 bp
02: gap of 100 bp
13280: contig of 978 bp
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17072: contig of 849 bp
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8479: contid of
8579: gap of 10
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AC012230 175064 bp DNA linear HTG 22-APR-2000
Homo sapiens clone RPll-1Ml0, WORKING DRAFT SEQUENCE. 39 unordered
pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                3154 TTGTTTCGAGGCCAAGGAGGCTTCGGGAAGTGCTCGGTTTCGGGGACTTTGATCCGGAGC 3213
                                                                     41705 CCCGGTTCTGT/TTTTCTCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAAGACACGC
                                                     Sequencing vectors M13, M78815; 100% of reads Sequencing vectors M13, M78815; 100% of reads Chemistry: Dye-terminator B10 bye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 117571 bases at least Q40 Consensus quality: 160940 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
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Insert size: 171264; sum-of-contigs
Quality coverage: 2.9 in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-1M10
Unpublished
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Web site: http://www-seg.wi.mit.edu
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Center clone name: 1_M_10
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l (bases 1 to 175064)
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AC012230.3 GI:7637254
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41883 CC 41884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2435 CCCTCCCTCCGGCTGAGGAAACTAACAAA-GGAAAAAAATTGCGGAAAAAATTTA 2493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2494 GAGGAAGCAAATTCCACTGGTGCCCTTGGCTGCCGGAACGTGGACTAGAUAGTCTGCGG 2553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2614 GGGAGGCAGACCGCGGACCCTAAGACACCTGCTGTACCCTCCACCCCACCCCACCCCAC 2673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2674 CCACCTCCCCCAACTCCCTAGATGTCTTGGCCCCCTGAACGTCACCTCGTTTAAGGGG 2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2854 AGCCGAATCTATAAAAGGAACTAGTCCCGGCAAAAACCCCGTAAT GCGAGCGAGTGA 2933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2974 GCGGGGGGCTCCGCGCACCACAGAGCCGGTTCTCAGGGGGGGCTTTGCTTGTTTTTC 3033
                                                                                                                                                                                                                                                                                                                                                                                                                                                              7: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGGGGGGGGAGGAGGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTGCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2914 GTGGGGCCGGGACCCGCAGAGCCGAGCCGACCCTTCTCTCCGGGGC1GCGCCAGGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 69570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                indels
                                                                                                                                                         60120: gap of 100 bp
60983: contig of 863 bp in length
61083: gap of 100 bp
61935: contig of 852 bp in length
62035: gap of 100 bp
62056: contig of 831 bp in length
                                                                                                                                                                                                                                                  62966: gap of 160 bp
63827: contig of 861 bp in length
                                                                                                30: gap of 100 bp 59082: contig of 852 bp in length
                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                         66684: contiq of 844 bp in length
                                                                                                                                                                                                                                                                                                                                                                     66784: gap of 100 bp
67651: contig of 867 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 699.8; DB 2;
Pred. No. 4.1e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
       55329: gap of 100 bp 55139: contig of 868 bp in 5629: gap of 100 bb 57163: contig of 866 tp in
                                                                  57263: gap of 100 bp
58130: contig of 867 bp in
58230: gap of 100 bp
                                                                                                                             59182: gap of 100 bp
60020: contig of 838 bp in
                                                                                                                                                                                                                                                                                127: gap of 100 hp
64783: contig of 856 bp in
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                                                                                                                                                                                                                                               160 bp
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contiq of
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65740: cont
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pleces is not known and their order in this sequence lecord is Quality coverage: 3.2 in Q20 bases; sum-of-contigs 185: gap of 100 by 100 by 986: contig of 1994 bp in length 979: gap of 100 bp 986: contig of 1707 bp in length 12253: contig of 2467 bp in length 12353: gap of 100 bp 11353: gap of 100 bp 15353: gap of 100 bp 160 p of 100 bp in length p of 1270 bp in length p of 100 bp contig of 1994 bp in length p of 100 bp in length contig of 1707 bp in length 221: gap of 100 bp 22587: contig of 2356 bp in length 587: gap of 100 bp 1003: contig of 1003 bp in length 1004 1103: gap of 100 bp 1104 2634: contig of 1531 bp in length 2635 2734: gap of 100 bp 2635 2734: gap of 100 bp of 100 tp contig of 1681 bp in length 28284: gap of 100 bp 31338: contig of 3054 bp in length 31438: gap of 100 bp 34299: contig of 2861 bp in length 99: gap of 100 bp 38318: contig of 3919 bp in length 38418: gap of 100 bp 42835: contig of 4417 bp in length 45548: gap of 100 bp 48116: contig of 2568 bp in length 48216: gap of 100 bp 52618: contig of 4402 bp in length 18: gap of 100 bp 56592: contig of 3874 bp in length 56692: gap of 100 tp 59635: contig of 2943 bp in length 63761: gap of 100 bp 68437: contig of 4676 bp in length 68537: gap of 100 bp 71458: contig of 2921 bp in length ap of 100 bp contig of 5330 bp in length 76988: gap of 100 bp 82113: contig of 5125 bp in length 82213: gap of 100 bp 88220: contig of 6067 bp in length 120: gap of 100 bp 93499: contig of 5179 bp in length 17300: gap of 100 bp 20131: contig of 2831 bp in length 42935: gap of 100 bp 45448: contig of 2513 bp in length 35: qap of 100 bp 63661: contig of 3926 bp in length p of 100 bp contig of 4302 bp in length 103116: gap of 100 bp 109178: contig of 6062 bp 100 bp. f 5015 bp 100 bp 98001: gap of 1 103016: contig of gap of gap of 4415: con 4515: gap of 5785: con 97901: 76888: 12353: 15328: 25807: 52718: 20231: 59735: 71558: 93599: 34399: 9826 5885: 7979: 22687 31339 34300 20132

179 109278: qap of 100 bp 117307: contig of 8029 bp in length 1308 17407: contig of 8029 bp in length 1408 124079: contig of 6072 bp in length 180 131281: contig of 100 bp 180 131281: contig of 7102 bp in length 180 13181: qap of 100 bp 100 bp 180 13815: qap of 100 bp	iocation/Qualifiers 1. 175064 /organism-"Homo sapiens" /db_xref="taxon:9606" /clone="RP11-1MHO"	1003 note-*assembly_fragment* 104. 2634 note-*assembly_fragment* 735. 4415	ass 578 787 787 968	"assembly_fragment 17200 "assembly_fragment 17200 "assembly_fragment 20131 "20131 "assembly_fragment 20131 "assembly_frag	sembly_fra 5587 5707 5707 5707 5707 5800 5103 5800 51133 5800 5800 51299 5800 5800 5800 5800 5800 5800 5800 58	assembly_iragment. 42848 assembly_fragment. 48448 assembly_fragment. 55648 assembly_fragment. 55692 assembly_fragment. 56592 assembly_fragment.	"assembly- "assembly- "68437 "assembly- "71458 "assembly- end:S66:
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HOMO Sapiens clone RPII-1NID, DAW-PASS SEQUENCE SAMPLINE.
ACU21246
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Anderson, S., Baldwin, J., Barta, N., Berker Ly, E., Beela, E.,
Boguslavkly, L., Boukhqalter, B., Brown, A., Burkett, C., Pastie, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Gramiata, Verrebrani, Euteleostomi,
Mammakia, Eutheria, Primates, Catarrhini, Hominidse, Homo.
                                                                                 CCCAGATCGCACCATTGCACTCCAGCCTGGGCAACAAAGGTGAAACTCCATGTCAATTA 1559
                                                                                                                                                                                                                                                                                                                                                                                                                  62 CCCAGATCGCACCATTGCACTCCAGCCTGGGCAAAAAGGTGAAATCCATGTGAATTA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 TGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATANGALGGGAAAAA 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 CCAGGTACTIGGGAGGCTAAGGIGGGAGGAIGGCTTGAGGCCAGGGAGTCAAGTGTAACAG 631
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                                  Indels
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Birren,B., Linton,L., Nusbaum,C. and Lander, E.
.8; DB 2;
1.le-137;
                                U; Mismatches 107;
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Unpublished
Score 553.8;
Pred. No. 1.1
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17.1%;
84.0%;
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Homo sapiens.
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               Similarity
                                Matches 569;
Query Match
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Perteilano, K. Johnson, M. Doyle, M. Fenestor, J. Galagan, J. Ferretia, P. Fitzhugh, M., Forrest, C., Gage, D., Galagan, J., Gardyana, S., Grant, G., Hagos, B., Heafroid, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPhotters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Plerre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Sto, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teafaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Limmer A. and Zody, M.

Direct Submission

Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced g1:6705871.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.gucnome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generich and allows overlap relationships among clones to be deduced. NOTE: This record contains 73 individual sequencing reads that have not been assembled into However, it should not be assumed that this clone will be sequenced to completion. In the event that Collymore, A., the record is updated, the accession number will Jap of 100 bp in length 2: contig of 846 bp in length 2: contig of 880 bp in length 3ap of 100 bp in length 3: contig of 878 bp in length 100 bp in length contig of 841 bp in length of 100 bp routig of 851 bp in length contig of 851 bp in length gap of 100 bp 1834: contig of 863 bp in length 1: gap of 100 bp 2804: contig of 870 bp in length 100 bp f 870 bp in length 41: qap of 100 bp 15196: contiq of 855 bp in length 96: qap of 100 bp 871: contig of 871 bp in length 800 bp in length in length contig of 846 bp in length 100 bp of 844 bp in l 100 bp of 851 bp in L 00 bp i 14241: contig of 851 bp 100 bp 100 bp 100 contig of contig of contig of contig of contig of 176: gap of 11322: cont 14380: dap of 14 841: 4ap of gap of gap of 6640: gap of 7509: cor dap of gap of 5740: gap of 7609: gap of 8579: gap of gap of gap of 971: gap of Cent.er code: WIBR 9430: 4696 5640: 6540: 8479: 10376: 11323 11422: qap 11423 - 12302: 3745: 1 1280 2303 12402: 10476: 4796: 2904: 3845: 1934: 9530: be preserved 872 972 1835 1935 2805 3746 7510 7610 8480 10 177 1177 2905 1845 4697 4797 5641 6541 0838 10477 6641

15296: 4ap of

in length in length in length in length		in length	is length. In length.	in length
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16123: cont.ig 16223: gap of 17072: cont.ig 17172: gap of 18041: cont.ig 18041: gap of 1909: cont.ig	6: 940:	2662[: co 6721: gap o 7676: 99a o 28532: gap o 2842: gap o 9592: 9ap o 31410: co 31410: co 331410: co 33141: gap o 3312: gap o 4368: co	35204. 633204. 53304. 53	42013: gap of 42824: contig 4376: contig 4376: contig 44752: contig 4452: gap of 4524: gap of 46643: contig 4673: gap of 46643: gap of 4659: qap of 4651: contig 4855: gap of 4865: contig 4865: gap of 4865: contig 4865: contig 49185: contig 49185: contig 49185: contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Pukaryota, Metazoa; Chordata; Craniata; Vertebrata; Futbleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidac; Homo.
1 (bases 1 to 90698)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-24J9
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Submitted (16-JAM-2000) Whitehead Institute/MII Genter for Genome
Research, 320 Charles Street. Cambridge, MA 22141. USA
on Jul 13, 2000 this sequence version replaced q1:5705761.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ttp.genome.washington.edu/HM/krq-atMasker.ltm]
Center: Whitehead Institute/ MTH Center for Genome Research
                                                                                                                                                                                                                                                          90698 bp DNA Librar FIG : Homo sapiens clone RPI1-24J9, LOW-PASS SECTENCE SAMPLING, AC021345.
AC021345.2 GI:9130845
HTG: HTGs birent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions%genome.wi.mit.edu
------- Project Information
Center project name: L4483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlap relationships among clones to be deduced. However, it should not be assumed that this close will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the record is updated, the accession number will be preserved.
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33 38502; gap of 100 bp 139802; contiq of 878 bp in length 139480; contiq of 978 bp in length 139480; contiq of 927 bp in length 18405; contiq of 989 bp in length 14055; gap of 100 bp 
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60058: contiq of 883 bp in length
60158: gap of 100 bp
61067: contiq of 909 bp in length
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44356: contig or 899 bp in length
44456: gap of 100 bp
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53205: contig or 884 bp in length
54225: contig or 920 bp in length
54225: contig or 920 bp in length
25: gap of 100 bp
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65975: contiq of 860 bp in length
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67947: contig of 893 hp in length
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69910: contig of 876 bp in length
70010: gap of 100 bp
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55206: contig of 881 kp in lenath
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66954: contig of 879 bp in length
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63022: contig of 87: tip in
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Query Match 14.8%; Score 478.8; SB 2; Lenath 90698; Best Local Similarity 90.8%; Pred. No. 1.6e-117; Matches 543; Conservative 0; Mismatches 49; Indels 5: Gaps 7; Conservative 0; Conserva

10144 CCGGGCATGGIGGCAGGTGCCTGTAATCTCAGCTAGTGGGAGGTGGAGGTTGCAATGAG 10203 241 421 4.8.1 482 CCCTGTCTACAAAAAAAAAAAAAAAATTAGATGGGTGTGGTGGCATGCACCTGTGGTC 541 542 CCAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCCAGGGAGTCAAGTCTAC 599 CCCAGATCGCACCATTGCACTCCAGCCTGGGCAACAAAAGGTGAAACTCCATCTCAATTA 182 GATGGAGGGTCAGGGAGATCTAATTACTCTCTAAAATCATGCTAGGAAAGATAACACCTT 362 AGATGAAGAAACAGGCCGGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGGAGGC 422 TGAGGCCAGAGGATGGCTTGAGTTCCAGAGTTTGAGACCAGCCTGGATAACATGGCAAAA 62 qq qq g qq ò g ò Ωp ò g ò ŝ င် ŝ ें

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OLIGO\_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

2054640 seqs, 14551402878 residues Searched:

Word size ;

90539 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 20000000000 DB DB Minimum Maximum I Post-processing: Listing first 1000 summaries

GenEmbl:\* Database :

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AF258627 Homo sapi AC004139 Homo sapi AL807243 Mus muscu AC021850 Homo sapi AF287263 Mus muscu AC103824 Homo sapi AC107569 Homo sapi AL023575 Human DNA AL049113 Human DNA Sequence Sequence Homo sapi Homo sapi Human DNA Homo sapi Homo sapi Homo sapi Homo sapi Sequence Homo sapi Homo sapi Sequence Sequence Homo sapi Homo sapi Human DNA Description AC021345 H AF258627 H AC004139 H AX060894 AC012230 AC015494 AC015494 AC015494 AC015495 SUMMARIES AX351031 AX351029 AF287262 AF275948 AL359182 AX092589 DΒ Length .1 186889 .1 206966 .1 278572 149034 96717 183999 1643 1643 175064 175064 69570 90698 697 126295 201144 100.0 1000.0 60.5: 39.7: 30.8 28.1: 18.7 18.7 18.7 18.7 Query Match Score Kesult ş

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oy ob	1981 AATITTACAGGACTGCAATICTCTGGCCTGCACATGTATACAAGGGAATACAA 2040 	KEYWORDS SOURCE Homo sapiens ORGANISM Homo sapiens Eukaryota, M	Homo Sapiens. Homo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Suteleostomi;
à cả	2041 GTCCTGTGTTTTTATCACAGGGGCCTGATCAATATAATGAAATTAAAAGGGGGCTGGTG 2190 	Mammalia; REFERENCE 1 (bases AUTHORS Qiu,Y., C TITLE Human and	Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo. 1 (bases 1 to 201144) Qiu,Y., Cavelier,L., Chiu,S., Yang,X., Rubin,E. and Cheng,J.F. Human and mouse ABCAl comparative sequencing and transgenesis
c c	210) CATALIGHTCHGHOTTTHTGHTHGHTHTGHTHCHHTHTHTHTHTHTHTHTHTHT		evealing nove: regulatory sequences 73 (1), 66-76 (2001)
o co	2161 TCCTTCCTCTAATTTATGAAGAGAGTAGTACTTCCTCTGGGTCCTCTGGGGA 2220 	KEFERENCE 2 (Dases AUTHORS Qiu.Y., Ca TITLE Direct Sub JOURNAL Submitted	<pre>1 to 201144) avelier.L. Chiu,S., bmission (13-JUL-2000) Genome</pre>
oy Cp	222) CCFGGGGAGCTCAGCTGGGAATCTCCAAGGCGCTATCCAAAATCAAAGTC 2280 11111111111111111111111111111111111	Berkeley CA 94720, FEATURES SOUTCE	National Laboratory, 1 Cyclotron Rd, MS 84 USA Location/Qualifiers
ç 5	2281 CAGGTITGTGGGGGAAAACAAAAGCGCCATTACCCAGAGGACTGTCCCGT 2340 2281 CAGGTITGTGGGGGAAAAAAAACAAAAGTTACCCAGAGACTGTCGCCT 2340		nism+"Homo saplens" ref*"taxon:9606" .181457 -*ABCA1"
cy Op	2341 CACCCCAGCCTTGGAAAGGAAACAAAAAGGAAAATGATTGGCG1CCTGA 2400 11111111111111111111111111111111111	∃K <b>NA</b>	join(33931. :34151,58319. :58476,72893. :72986,77520. :77661 78931. :79046,101040. :101169,104152. :104328,117287. :11737 122329. :122569,125285. :125424,125554. :125870, 130079. :130276,131023. :131228,131749. :131925,
Oy Db	240) GGGAGATTCAGCCTAGAGCTCTCTCCCCCAATCCCTCCGGCTGAGAAACTAAC 2450 		133708. 133930,135677. 135898,136659. 137163. 138268. 13891,140179. 140350,141340. 141471. 142777. 142919,143123. 1443260,143663. 144183. 145441. 145513,146657. 146859,148527. 148575.
AG qu	246) AAAGGAAAAAAAAATIGGGGAAAGGGGATTTAGAGGAAGGA		.148884,150280, 159428,1520/8. .15536,156568. 156757,18278 .159714,160837. 160942,162417. .165182,164413. 164590,166588.
oy op	2521 addTGCCGGGAACGTGGACTAGAAGTCTGCGGCCCGAAACCGGAACGGTTCCGGC 2580 		. 170229, 171017 17079, 1713987
cy Sp	2581 GCGTCTTAGGCCGCGGGCCCGGGCGGGGGGACGCAAMMCGGGAMMCTTAGAGACA 2640 FILLITITITITITITITITITITITITITITITITITIT	exon	SCAL" "ATP-binding 14151 SCAL"
Oy Dp	2641 CCTGCTGTACCCTCCACCCCACCCCACCCCACCCACCCAC	exon	476 A1"
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Q Q	2761 IGAGTGACTGACTACATAAACAGAGGCGGGAAGGGGGGAGGAGGGGAGAGAGCACAG 2820 		135/08. 133930,1356/7. 135881,136959. 137163, 138268. 138381,140179. 140350,141340. 141471, 142777. 142919,143123. 143260,143963. 144183, 145441. 145513,146657. 146859,148527. 148575,
0y Db	2821 GCTTTGACCGATAGTAACCTCGGGTTGGGGGGGGAATCIATAAAAGGAACGAGTC 2889 		.48884,150280, .150428,152078, .1 151536,156568, .156757,158278, .1 159714,160887, .160942,165417, .1 163182,164413, .164590,166588, .1
δ	2681 CGGCAAAAACCC 2893		166815. 166959,168505. 168628,169715. 16984, 170109. 170229,171017. 171079,171987. 172093, 174448. 174589,174961. 175095,176039. 176142,

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31069 GGCCATGGTGGCAGGTGCCTGTAATCTCAGTTACTCGGGAGGTGGAGGTTGCAATGAGCC 31128
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BEKUGKVGEMAIRKLGLYVCEKYAONYSGGNKHKLSTAMALIGGPPVYFLDEFTIG
MDPRANFELMRCALSVKEGRSVYTTSHSMEELEAICTRMAIMVNGRPRCLGSVVGHLK
NRFGDGYTIVVRIAGSNPDLKPVQDFFGLAFPGSVLKEKHHNMLQYQLPSSLSSLARI
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SYPPYEQHECHFPNKAMPSAGTLPWVQGTTCNANNFFFRYTTGGEAPGVVGNFNKSIV
ARLFSDARRILLYSQKDTSMKDMRKVLRTLQGTKKSSSNLKLQDFLVDNFTFSGFLYH
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Joses 1 to 149034)
Santamarina-Fojo,S., Peterson,K., Knapper,C., Qiu,Y., Freeman,L., Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C., Prades,C., Chimini,G., Blackmon,E., Francois,T., Duverger,N., Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete genomic sequence of the human ABCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
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                                                                                                                                                                                1384 TATGCGFCTGTCCTGAGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGCCGTG 1443
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Santamarina-Fojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A.,
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                               1504 AGGTGGTGGGAGTTCTGGAATATGATGGAGCTGGAGGTGGGAAGAAGAAGTAGGGG
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/organism="Homo sapiens"
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Submitted (1: JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CBO 18A, UK. E-mail enquirles:
hamproyyssanger.ac.uk Clone requests: clonerequestésanger.ac.uk
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                                                          2221 CCTGGGGAGCTCAGGCTGGGAATCTCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTC
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                                                                                                               /rpt_family~"HERV"
61246. .61489
                                                                                                                                                                                        /rpt_family-"Alu"
64082, .64306
                                                                                                                                                                                                                                                                                                         /rpt_family*"Alu*
69481. .69760
                                                                                                                                                                                                                                                                                                                                              /rpt_family."Alu"
71998. .72233
                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family-"Alu"
72244, .72501
            /rpt_family-"Alu"
55297. .55344
                                                      /rpt_family."Alu"
58501. .58935
                                                                                                                                                   /rpt_family-"Alu"
62812. 63077
                                                                                                                                                                                                                                /rpt_family="Alu"
67123. .67382
                                                                                                                                                                                                                                                                     /rpt_family="Alu"
68499. .68731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0:
                                                                      58935
/note="LTR"
                                                                                                                                                                                                                                                                                     .68731
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corresponding to the overlapping clone, as we sufficiely administration only a small overlapping a show.

This sequence was finished as follows unless otherwise noted: all requions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all requions were covered by at least one plasmid subclone or more than one MIT subclone: and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary series on numbers alive the feature table with their source databases: Em., EMBL; SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpop This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/HGP/Chr9
RP11-217B7 is from the library RPCI-il.1 constructed by the group
of Pieter de Jonq. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from a single pur clone, Restriction digest data confirm the assembly."
On Jan 15, 2002 this sequence version replaced gi:18121468.
During sequence assembly data is compared from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derived from a single post clone. Restriction digest data
                                                                                              together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sections only once, except for a short overlap.

The true right end of clone RF12.21787 is at 557.7 in this sequence. The true left end of clone RP11-122F10 is at 72980 in this sequence. The true right end of clone RP11-132F0 is at 2000 this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISSPROT; IT:, TREMBL; Wp:, WORMPEP; Intermation on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Sequence it as reads that a shart insert library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Sequence from reads from a smoot insert library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              829 TGTCAAGTITGACCCCAAAACCCAAIITATIGACCAAGGFTAITGTTTGACTGAGGCAAG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Sequence from overlapping clone RFI1-122F16
(ACO26643). Assembly continued by restriction digest.
                                                            Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anote-"Sequence from AF27594% sequenced by National Institutes Of Health National Health. Uniq and Blood fortices has been an 2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RPI1-217B7 It may be shorter because we sequence everlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              769 AGAAAAAAACAAGATGAAACAGGGGAGAAAGACHTTAGGTAAATTGGTGATGTGGT
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Institute, Bethesda, MD 20892, USA.
84249. .84273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 9, constructed by the Sauger Cent
Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%; Score 891; DB 99.7%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:5606"
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3238. .3278
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Matches 1041; Conservative
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PAT 21-MAR-2001
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19314 TGTCAAGTTTGACCCCAAAACCCAATTTATTGACCAAGGTTATTCTTTGACTGAGGCAAG 19255
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                                                                                                                                                                                                                           18774 IGCTIGGGCCTCIICTAIGGGTCIGTGAGTGTTGATAGAACCACTGATGIGAGTACC 18715
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                                          AICCCTTTCTTTTAFTTTCTTGACACGGAGTCTTGCTCTGTCACCTCAGGCTGGAGTGC
                                                                                                       19194 ATCCCTTICTTTTATTTTTCTTGACACGGAGTCTTGCTCTGTCAGGCTGGAGTGC
                                                                                                                                                  AGTGGCATGATCTCCACTCTAAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCC
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                            889 GGGTCCCCTCTCTGGGCCTTGGGCTTTAGAAAGCTCATCTCTGGCCTTTCTGAGATCC
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AX092589
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo. 1 (Dases 1 to 18399) Hayden, M. Brooks Wilson, A. R., Finstone, S. N. and "lee, S. N. Compositions and methods for modulating hdl cholesterol and triplyceridal levels triplyceridal levels University of British Columbia (CA); Xenon Genetics Inc. (CA)
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AF25862351 1167 bp DNA linear PRI 23.JUN-2000 Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23.JUN-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, San Francisco, CA 94143-0130, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               27511 AATGIGAATCTGCCCTTCAAGGTGGCIACAAAGGTATCTTTGTCAAGGTAGGAGCCTTG 27570
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AATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGACGCCTTG
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Vallinger.C.R. Hakamata,H., Duchateau,P.N., Eng.C., Pielding,C.J. and Kane,J.P.

Analysis of haBCl gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

Biochim. Biophys. Res. Commun. 271 (2000) In press

(bases 224 to 1167)

Aullinger.C.R. Hakamata,H., Duchateau,P.N., Eng.C., Direct Submission
                                                                             Sequence update by submitter
On Jun 23, 2000 this sequence version replaced g1:7769713.
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[ (bases 1 to 1167)
Porsch-Ozcurumez,M., Langmann,T., Hohnerl,S., Borsukova,H., Kaninski,W. E., Drobnik,W., Hohnerl,S., Schumadich: G. and Schmitt,G. of ATE ainc tinger protein 202 (ZMF202) is a transcriptional repressor of ATE binding cassette fransporter Al (ARCA); and ARCGI gene expression and a modulator of cellular ligid efflux 206 (15), 12427-12448 (2001)
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                          2250 GGCAGTAGGTCGCCTATCAAAATCAAAGTCCAGGT1TGTGGGGGGAAAAAAAAGCAGC 2309
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transporter-1, 5'UTR and promoter region.
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AJ252201.1 GI:12053757
ABC-1 gene; ATP-binding cassette transporter-1; promoter
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/db_xref="taxon:9606"
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1. .1167
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Porsch-Oezcueruemez,M.K.
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1, 942
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                                                                                     //function-"cholesterol efflux regulatory protein" 315 c 327 g 247 t
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/function="cholesterol efflux regulatory protein"
896. .900
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Mammalia, Eutheria, Primates, C<mark>atarrhini, Hominidae, Ho</mark>mo
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Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abcl
Patent: WO 0078972-A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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Pred. No. 2.6e-293;
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Sequence 3 from Patent WO0078972.
AX060715
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                               /gene-"ABC-1"
                                                                    /gene-"ABC-1"
                                                                                                                                                                                                 Matches 541; Conservative
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1 (bases 1 to 1643)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abol polypertidus
Patent: WO 0078971-A 3 28-bEC-2000;
CV THERAPEUTICS, INC. (US)
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                                                     100.0%; Pred. No. 2.5e-293; ive 0; Mismatches 0;
                                          Score 541; DB 6;
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/db_xref-"taxon:9606"
413 c 457 g 40
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/db_xref-"taxon:9606"
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                                            18.78;
           413 c
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Matches 541; Conservative
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Score 541;

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldain, J., Barna, N., Beckerly, R., Boyuslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Down, Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gardon, C., Hardon, L., Hardon, L., Hardan, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Connell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stanuc-Thomaun, N., Stojanovic, N., Subramanian, A., Talamas, J.,
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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1274 GAAGGGACGCACCGGGACCCTAAGACACCTGCTGTACCTCCACCCCACCCCACC 1333
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-1M10
100.0%; Pred. No. 2.6e-293; tive 0; Mismatches 0;
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AC012230.3 G1:7637254
HTG: HTG:_PHASE1; HTGS_DRAFT.
HOM: SAPIENS.
  Best Local Similarity 100. Matches 541; Conservative
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TITLE JOURNAL COMMENT

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97902 98001; qap of 100 bp 97902 98002 103016; cont.ig of 5015 bp in length 10317; 10316; gap of 100 bp 10317; 109278; cont.ig of 6062 bp in length 10917; 109278; qap of 100 bp 117408 124079; cont.ig of 6672 bp in length 117408 124079; cont.ig of 6672 bp in length 124080 124179; gap of 100 bp 124180 131281; cont.ig of 100 bp 13182 131381; gap of 100 bp 13182 131381; gap of 100 bp 13182 131381; gap of 100 bp 131382 131382 138059; conf.ig of 6678 bp in length 131382 1318059; conf.ig of 6678 bp in length
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145592 157391: contiq of 11800 bp in length
157392 157491: gap of 100 bp
157492 175064: contiq of 17573 bp in length
                                                                                                                                                                                                                                          68437: contig of 4676 bp in length 5377: gap of 100 bp 71458: contig of 2921 bp in length 558; gap of 100 bp 76888: contig of 5330 bp in length 76888: contig of 5330 bp in length 76888: contig of 5330 bp in 100 bp 
                                                                                                                                         qap of 100 bp
35: contig of 2943 bp in length
aap of 100 bp
51: contig of 3926 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82213: gap of 100 bp

88220: contig of 6007 bp in length

88320: gap of 100 bp

9349: contig of 5179 bp in length

9359: gap of 100 bp

97901: contig of 4302 bp in length
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138160 145491; contig of 7332 bp in length
                           116: gap of 100 bp
52618: contig of 4402 bp in length
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contig of 5330 bp in length
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48116: contig of 2568 bp in length
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                                                                                        18: gap of 100 bp
56592: contig of 3874 bp
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12354. 15228
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/note-"assembly_fragment"
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/note-"assembly_fragment"
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Zuote-"assembly_tragment"
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Znote-"assembly_fragment"
17301 20131
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/cote-"assembly_fragment"
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/sote-"assembly_tragment"
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/sote *assembly_tragment*
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                                                                                  Submitted (21-OCT-1999) Whitehead Institute/MII Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, 35A on APT 22, 2000 this sequence version replaced qi:6454333. All repeats were identified using RepeatMassec.
                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary, Gaps between the conflor are represented as funs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                         Smit. A.F.A. & Green, P. (1996-1997)
Littp://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                   100 bp
of 1531 bp in renath
100 pp
of 1681 bp in length
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22587: contiq of 2.6% bp in length
22687: gap of 136 bp
25707: contiq of 9820 bp in length
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1004 1103: gap of 100 bp
1104 2634: contig of 1531 bp in length
2535 2734: gap of 100 bp
2735 4415: contig of 1681 bp in length
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4516 5785; contra of 1270 bp in length
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7879; centig of 1994 bp to length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31438: gap of 10, np
34299: contig of 280; up in length
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38318; contig of 4919 hp in length
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contin of 4417 bp in length
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Web site: http://www.seq.wi.mit.edu
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17200: cont
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With the state of 
                                                  AC012230 175064 bp DNA linear HTG 22-APR-2000
Homo sapiens clone RPI1-1MIO, WORKING DRAFT SEQUENCE, 39 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Whitehead Institute/ MJT Center for Genome Research
Center code: WBB
Web site: http://www.seq.wi.mit.edu
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1004 1103: gap of 100 bp
1004 2634: contig of 1531 bp in length
2635 2735 2735 contig of 1681 bp in length
2735 2735 contig of 1681 bp in length
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Center clone name: l_M_10
                                                                                                                                                                        HTG: HTGS_PHASE1: HTGS_DRAFT.
Homo sapiens.
Homo sapiens
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1 (bases 1 to 175064)
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AC012230.3 G1:7637254
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RESULT 12
AC012230/c
LOCUS
                                                                        DEFINITION
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9865: 9ap of 100 bp 799; 9ap of 100 bp 9186; 9ap of 100 bp 1253; contiq of 1944 bp 1253; contiq of 1945 bp 1253; contiq of 2467 bp 1253; eap of 100 bp 15328; gap of 100 bp 17300; contiq of 2875 bp 17300; contiq of 2831 bp 17300; gap of 100 bp 18484; contiq of 2402 bp 18484; contiq of 2513 bp 18548; gap of 100 bp 18558; gap of 100 bp 18558; gap of 100 bp 18569; contiq of 2313 bp 18561; contiq of 2313 bp 18501; gap of 100 bp 18761; gap of 18631; contiq of 17571 bp 188059; contiq of 17571	4 + 1 00	Telliden	a lenath	n leogth		n lengtr	n length	4	-	n lenath	n Denath		a leagth	n length		-	n length	r length	-	c Length	n jength	n length	, ,	n length	n length	n jesath	-		n length	n length	ո Դորգ։ Ե		- Fellow 1	n endts.	n jength	n length	Ç	J.	n length	n lengtt.		n length	n length	-	<u> </u>	in length	in length.		
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Gaps . 0 Length 175064; Indels /clone="RP11-1M10" /clone\_lib="RPCI-11 Human Male BAC" 11.9%; Score 344; DB 2; I ilarity 99.7%; Pred. No. 6.1e-182; Conservative 0; Mismatches 1; 34400. .38318 /note-assembly\_tragment\* 38419. .42835 /note-assembly\_fragment\* 42936. .4548 /note-assembly\_fragment\* 45549. .48116 /note-assembly\_fragment\* 17301. 20131 /note assembly\_fragment 20232. 22587 /note assembly\_fragment 22688. 25707 /note assembly\_fragment 25808. 28184 /note assembly\_fragment 7980. 9686 /note assembly\_fragment 9787. 12253 /note assembly\_fragment 56693. 59635 /note-"assembly\_tragment" 59736. 63661 /note="assembly\_fragment" 1104 2634 /note="assembly\_fragment" 12354. 15228 /note-"assembly\_fragment" 15329. 17200 /note-"assembly\_fragment" 48217. .52618 /note="assembly\_fragment" 52719. .56592 /note="assembly\_fragment" /note="assembly\_fragment" 63762. 68437 /note="assembly\_fragment" 2735. 4415 /note="assembly\_fragment" /note-"assembly\_fragment" 68538. 71458 /note-"assembly\_fragment /db\_xref-"taxon:9606" clone\_end:SP6 / vector\_side:left" 71559. .76888 Query Match Best Local Similarity Matches 394; Conserv misc\_feature ò qq ò a a ò

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However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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All repeats were identified using RepeatMusker.
Smit, A.F.A. & Green, P. (1996-1997)
Http://ftp-genome-washington.edu/RM/RepeatMusker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 69570)
                Center: Whitehead Institute/ MIT Center for Genome Research
                                                               275 TGCCAAGGAGGTCCAAAGGTTTCAACAAAGFTCAGTFTCAGAAAAAACCTTTGAGGAAGAG 334
215 AAATCATGCTAGGAAAGATAACACCTTTTAATAACACTGGTGGTGTTTATAAGATCATGC 274
                                                                                                                                    335 AGAATATACATCTICTCTCCATTTTAAAGATGAAGAAGAAGGGGGGGGGAGAATGAGTAAT
                                                                                                                                                                                                                                                                                                                                          Homo sapiens clone RPIi-INIO, LIW-PASS SEQUENCE SAMPLING AC021246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful to identifying clones that may be generich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome, clone RP11-1N10
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                                                                                                                                                                                                                                                                                                                                   ONA
                                                                                                                                                                                                                            395 GCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCCA 429
                                                                                                                                                                                                                                                                                                                                 69570 bp
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Center clone name: 1_N_10
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HTG; HTGS_PHASE0.
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2: gap of 4268: conti- 8: gap of 5204: conti- 4: gap of	6156: contin 6: gap of 7128: contin 8083: contin 3: gap of 9031: contin 1: gap of	40006: coi 06: gap or 40967: coi 40967: coi 413: gap or 13: gap or 428:4: coi 76: gap or 76: gap or	3: qap ot 7559: conti 9: gap of 1485: conti 1485: conti 6: gap of 0: 440: conti 0: qap of 1404: conti 1404: conti 2: qap of 2: qap of	53328: cc 3428: gap o 5428: gap o 5529: cc 5529: cc 55197: gap o 57163: cc 7263: gap o 58130: cc 58130: cc 58130: cc 58130: cc 58130: cc	60983: contig 60983: gap of 60983: gap of 62865: contig 62866: contig 62966: gap of 63927: gap of 64783: contig 65840: contig 65840: contig 6684: gap of 66781: contig 67651: contig
333 344 426 520 520	530 615 712 722 722 903	0000 0000 0000 0000 0000 0000 0000 0000 0000	6644 6770 770 770 770 770 770 770 770 770 77	22244433444334443344433444333333333333	601021 601021 601036 601036 601036 601036 601036 601036 601036 601036 601036 601036 601036 601036 601036 601036 601036
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RS Bitren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Roderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,

Boduslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

DeArtellano, K., Dewart, K., Domino, M., Doyle, M., Fenestor, J.,

Ferreira, P., FitzHugh, M., Forrest, C., Gage, D., Galagan, J.,

Rardand, J. C., Johnson, R., Jones, C., Lug, C., Lug, C., Lug, C.,

Landers, T., Lehoczky, J., Levine, R., Liu, C., Lug, C., Lug, C.,

McPheeters, R., Meldrim, J., Meneus, L., McKernan, K.,

McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J.,

Norman, C. H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,

Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Tkuman, N.,

Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Tirell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, M. J.,

Zimmer, A. and Zody, M.

Direct Submitted (16-Jan-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:6705761.
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Birron, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-24J9
                                                                                                                                                                                                                                                                                                                             41199 TGCCGGGAACGTGGACTAGAGACTCTGCGGCGCAGCCCCGAGCGCTTCCCGCGCG 41258
                                                                                                                                     DD 41139 GGAAAAAAAAATGCGGAAAGCAGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGC 41198
                                                                                                           2464 GGAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTTGGC 2523
                                                                                                                                                                                                                       2524 TGCCGGGAAMGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCGCTTCCCGCGCG 2583
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  Length 69570;
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Score 156; DB 2; Length 699
Pred. No. 7.6e-76;
0: Mismatches 1; Indels
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Center clone name: 24_J_9
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                            Best Local Similarity 99.5
Matches 206; Conservative
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Figure Clones that may be query for any early than clones that may be query to be deduced by relationships among clones to be deduced as a gradient of the property of the pro	for S¥S	· 4	=																																								
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	rier	ever,	reco	prese	6	97	6	22	08	0 6	91	76	76	86	4.4	75	75	985	075	173	274	284	381	468 478	566	576	577	777	878 878	963	063	162	172 258	268	366	455	552	507 648	658	756	856 856	946 956	770

28 43457: gap of 100 bp 58 44356: contig of 899 bp in length 57 44456: gap of 100 bp 7456: gap of 100 bp 74525: contig of 869 bp in length 6 45425: gap of 100 bp 6 46305: contin f 26, 45425; gap of 4605; cont.go of 800 bp in length 4605; cont.go of 800 bp in length 47302; cont.go of 800 bp in length 1402; gap of 100 bp in length 1402; gap of 100 bp in length 1402; gap of 100 bp in length 140393; cont.go of 801 bp in length 150250; cont.go of 802 bp in length 150250; cont.go of 803 bp in length 150350; cont.go of 803 bp in length in length 66954: contig of 879 bp in length 194; dap of 100 bp E7947; contig of 893 bp in length in length in length in length in length 7522: 940 of 100 bp 18402: contig of 880 bp in 8602: 940 of 100 bp 39380: contig of 878 bp in 9480: 9407: contig of 927 bp in 10507: 9407: contig of 898 bp in 1505: 940 of 100 bp 41405: contig of 898 bp in 1505: 940 of 100 bp 42399: contig of 894 bp in 2499: 940 of 100 bp 43357: contig of 858 bp in 14357: contig of 858 bp in 14357: contig of 858 bp in 14357: contig of 858 bp in 143557: contig of 858 bp in 14357: contig of 32452: contig of 899 bp ir 3447: contig of 895 bp ir 3447: contig of 895 bp ir 3547: gap of 100 bp 34485: contig of 888 bp ir 4535: gap of 100 bp 5533: qap of 100 bp 16440: contig of 892 bp ir 16440: contig of 882 bp ir 16440: contig of 907 bp ir 37522: 62152 6302 63023 63122: 35533: 36540: 38502: 67054: 19480: 61068 61167: 61168 620 62052 62151: 40507 41505 54.226 54.326 55.207 3334448 34448 344436 34536 35534 35544 36541 37523 37524 37523 37523 37523 37523 37523 37523 37523 40508 40508 41406 41506 42400 43358 44457 444357 44457 44457 45426 45426 47403 47403 47403 47403 47403 47403 47403 47403 47403 47403 47403 47403 47603 51210 51310 52222 52322 53206 53306 55.107 56.166 56266 57125 57225 58122 58222 60159

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Cranidla, Verrebrata, Eutoleostomi,
Mammalia, Eutheria, Primates, Catariano, Homonidue, Hono.
                                                                                                                                                                                                       215 AAA1CATGGTAGGAAAGATAACACCTTITAATAA/ACTGTGTGTGTTTATAAVATGATTG 274
                                                                                                                                                                                                                                                             95 ACAAAAGGTGAAACTCCATCTGAATTAAAAAAAAAAAAGAATGTTTTSGTGGTGACTTCA 154
                                                                                                                                                                                                                                                                                                                                    355 AATAGGTAGGAGAAAGAAGGAGAGAGGAGAUGGTCGAGGGAGAICTAAIIACTCTCIA 214
                                                                                                                                                   Sdept 10
                                                                                                                                                                                    35 TACTIOGGAGGTGGAGGTTGCAATGAGGCCCAGAIGGCACCATTELACAIGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens ATP binding cassette transporter (AMCA1) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 697)
Pullinger,C.R., Hakanata,H., Dactateau,P.N., End.C.,
Advalcerat,H.E., Fleiding,C.J. and Kace,J.P.
Analysis of baBG1 gene? for enditional peptide sequence.
Promoter region, and four polymorphisms
Biochem. Biophys, Res. Commun. 27. (2000) in press
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/protein_id-"AAR69513.1"
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                                                                                                           Lemath 99,698
                                                                                                                                                2; Indels
67948 68047: gap of 100 bp
68048 68934: contig of 887 bp in length
                                68935 69034: qap of 100 bp 69035 69010: contiq of 876 bp in length 69911 70010: qap of 100 bp
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Pullinger.C.R., Hakamata,H., Eschateur.P.M.
Abnizerat,B.E., Fielding,C.J. and Kancel.P.P.
Öfrect Submission
                                                                                                             Score 152; DB 2;
Pred. No. 1.4e-73;
                                                                                                                                                0; Mismatches
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/db_xref="taxon:9606"
/chromosome="9"
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/gene="ABCA1"
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Submitted (14-FEH-1998) Whitehead Institute/MIT Center for Genome Submitted (14-FEH-1998) Whitehead Institute/MIT Center for Genome Steeperth, 420 charles Street, Cambridge, MA 02141, USA

Research, 420 charles Street, Cambridge, MA 02141, USA

Research, 420 charles Street, Cander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Butwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Collins, S., Collymore, A., Gage, D., Gardyer, K., Gerajery, K., Grant, G., Horton, L., Howland, J.C., Jacott, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdott, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdott, L., Molla, M., Morris, M., Morrow, J., Mychalecky, J., Nahf, R., Naylor, J., Nalle, M., Morrow, J., Nychalecky, J., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stanger Thomannia, P., Filwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella Hiller, I., Ve, W., H., Mark, M., Wheeler, J., Wuy, M., Y., Wyman, D., Peterson, J., Land, Zady, M., Rebeler, J., Wuy, M., Y., Wyman, D., Peterson, J., Muy, J., Wyman, D., Peterson, J., Muy, J., Muy, J., Wyman, D., Peterson, J., Land, Zody, M., Rebeler, J., Wuy, J., Wyman, D., Peterson, J., Muy, J., Wyman, D., Peterson, J., Wheeler, J., Wuy, J., Wyman, D., Peterson, J., Wheeler, J., Wheeler, J., Wuy, J., Wyman, D., Peterson, J., Wheeler, J., Wheeler, J., Wuy, J., Wyman, D., Peterson, J., Wheeler, J., Willey, W., Y., Wheeler, J., Wheeler, J., Willey, J., Wheeler, J., Willey, J., Wheeler, J., Willey, J., Willey, J., Willey, J., Willey, J., Wheeler, J., Willey, J., Willey, J., Willey, J., Willey, J., 
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Homo sapiens chromosome 17, clone HRPC843B9, complete seguence.
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/translation="MacWPQLRLLLWKNLTFRRQTCQLLLEVAWPLFIFLLLISVRL
SYPPYEQHECHFPNKAMPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVVGNFNKS"
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Submitted (02-SPP-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, 98A
on Sep 2, 1998 this sequence version replaced gi:3451370.
All repeats were identified using RepeatMasker: Smit, A.F.A. 6
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Homo sapiens chromosome 17, clone HRPC843B9
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/rpt_tamily="LIMEC" complement(1535315497) /rpt_family="L2" complement(1566215828) /rpt_family="MLTIG" complement(1630116607) /rpt_family="Alux" 1750017802 /rpt_family="Alux"	complement(18474. 18774) /rpt_family="AluSg" 18825. 18902 /rpt_family="MHR" complement(19656. 19771) /rpt_family="MER20"	1984. 2012, /rpt_family="AluSp" complement(2014520168) /rpt_family="(CAAAA)n" complement(2016920451) /rpt_family="AluSx" complement(2045620765)	complement(2102321343) /rpt_tamily=".i.M4" 2134421630 /rpt_tamily="A.usx" complement(2163121700) /rpt_tamily=".i.M4" 2229122526 /rpt_tamily=".i.M4"		complement(26630, .26725)  / Tpt_family="MIR" complement(26902, .26958)  / Tpt_family="(CA)n" / Tpt_family="CA)n" / Tpt_family="Alub" / Tpt_family="Alub" / Tpt_family="Alub" / Tpt_family="Alusq"		complement(33470, 33781) //pt_family=Aluyb8" complement(35504, .35774) //pt_family=LIME3A" 35830, .35906 //pt_family=AluJo" 35907, .36194 //pt_family=Aluy" 36204, .36516 //pt_family=Aluy" 36517, .36582 //pt_family=Aluy"
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Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.htm:. Location/Qualifiers 1126295 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="17" /map="17"	/clone_lib="Peter do Jong/ human PAC listary" complement(2, .193) /rpt_family="Alusx" complement(235, .410) /rpt_family="MERSA" complement(479, .640)	/rpC_ramily.*Mik. complement(7141012) /rpc_family=*Alusc* 11401269 /rpc_family=*I2* complement(25032646) /rpc_family=*MERSB* complement(26472954)	/rpt_family="AluJb" complement(29552998) /rpt_family="MER5B" 37584544 /rpt_family="L2" 47434873 complement(50685344)	/rpt_family="Aluyb" complement(64036675) /rpt_family="Aluyb" 67826950 /rpt_family="MIR" complement(7374) /rpt_family="Tigger!" complement(77357840)	<pre>/rpt_tanily='(GGA)n" complement(1841, .7876) /rpt_fanily="purine-rich" complement(7883, .7988) /rpt_fanily="rigger!" complement(7889, .8597) /rpt_fanily="rigger!" complement(8604, .8741) /rpt_fanily="rigger!" complement(86759, .9456) /rpt_fanily="rigger!" complement(48759, .9456)</pre>	Complement(940973) /rpt_family=Alusx complement(942010276) /rpt_family=Tigger!" /rpt_family=WRR47A" complement(1110611949) /rpt_family=L2 /rpt_family=L2 /rpt_family=L3 /rpt_family=L3	/rpt_family-"LIMC2" complement(130661322) /rpt_family-"L2" 132241325 132241325 1325213494 1325213494 1355213494 135613769 /rpt_family-"MIR" 140614334 /rpt_family-"MEK5A" complement(1483515195)
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07: gap of 100 bp
58284: contig of 2177 bp in length
184: gap of 100 bp
60786: contig of 2402 bp in length
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66707: contig of 5821 bp in length
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/note-"assembly_fragment:01920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Rodentia, Sciuroanathi, Muridae, Murinae, Mus.
1 (bases 1 to 186889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (29-JUN-2002) Wellcome Trust Sander Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Glone requests: clonerequestysanger.ac.uk
on Jul 2, 2002 this sequence version replaced 41:21568136.
                                                                                                                                                                                                                                                                                                                                        Db 31115 dates cache and a second control of the second control of
                                                                                                                                                                                                                                                                                          1017 GATCTCGACTCACTGTAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCC; AGCCTC 1076
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Consensus quality: 175959 bases at least Q40
Consensus quality: 179463 bases at least Q40
Consensus quality: 182069 bases at least Q20
Insert size: 184589; sum-of contias
Insert size: 18466; 5.5% error; adarosertp
Couglity coverage: 4.72x in Q20 bases; sum-of-contiay
coverage: 4.82x in Q20 bases; aquiose ip
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                                                                                               Length 126295;
                                                                                          2,2%; Score 65; DB 9; Length 126; 100.0%; Pred. No. 1.9e-24; rive 0; Mismatches 0; Indels
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40088 40187: qap of 100 bp
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p of 186 bp
contig of 6947 bp in length
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40188 44438; contig of 4251 bp in length
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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Matches 65; Conservative
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     repeat_region
                                                                                     Query Match
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KEYWORDS
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COMMENT

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SOURCE INFORMATION:
The FPC1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P. Y., Zhac, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial ciromsome libraries. Genomics 51:18 The clone may be obtained either from Research Genetics 1nc. (http://www.resgen.com) or pleter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The clone sequenced to the left is RPII-62B4. Actual start of this clone is at base position 1 of RPII-389E17; actual end is at base position 206966 of RPII-389E17.
                                 Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                           Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                            Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Feb 16, 2001 this sequence version replaced gi:11761497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapping information for this clone was provided by Fr. John D. McPherson, Department of Genetics, Washington University, St. L. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: H_NH0389E17
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                                                                                                                                                                   Direct Submission
Submitted (16-FEB-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:9606'
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3. .256
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/rpt_family="L1"
523. .1023
/rpt_family="L1"
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                                                                                                                    4 (bases 1 to 206966)
Waterston, R. H.
                                                                                                                                                                                                                                                           5 (bases 1 to 206966)
Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WUGSC
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                                                                                                                         KEFERENCE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0: Gaps
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Homo sapiens BAC clone RPI1·389R17 from 4, complete sequence.
ACO21850
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The sequence of Homo sapiens BAC clone RP:11-3895:17
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147175. 156317
/note="assembly_fragment:01564.0"
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Mismatches 0;
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                                                                                                                      /note-"assembly_fragment:00358
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Sulston, J.E. and Waterston, R.
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Matches 61: Conservative 0;
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Qiu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (14-JUL 2000) Genome Science Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Rd, MS 84-i71, Berkeley,
CA 94720, USA
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Eukaryota: Metazoa: Chordata: Sciurognathi: Muridae: Murinae: Mus.
1 (Dases 1 to 278872)
Oiu.Y., Cavelier, L., Chiu.S., Yang, X., Rubin, E. and Cheng, J.F.
Human and mouse ABCAl comparative sequencing and transgenesis
studies revealing novel regulatory sequences
Genomics 73 (1), 66-76 (2001)
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QNIJGRNISDYLVKTYVQIIAKSLKNKIWVNEFRYGGFSLGVSNSQALPPSHEVNDA

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.192475.
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176859,
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WEVSSLIPLLIVSAGLLVYIIKLGNILLPYSDPSVV;VFISVFAWTILOCELISTLESR
ANLAAGCGIIYFTTLEVYUCVAWDDYVGESIKIERDSTILSVAHGFGCEPALEEEG
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Birtet, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Marna, N., Hastlen, V., Boguslavkiy, L., Boukhqaiter, Brown, A., Camaratel, Canmopolano, A., Chang, J., Chazaro, B.,

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Ferretra, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,

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Viel, R., Vo, M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Parison, T., Peterson, M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Parison, T., Petherson, M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
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Homo sapiens chromosome 8 clone CTD-2319014 map 8, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                    TPVTKGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELL.TGRFHVEFFALLRGVPEKE
VGKGFWAIRKLGLYKYGEKYASNYSGNKRKLSTAMALIGGPVYFLDEPTTGMDPKA
PRETUMNCALSIVKEGRSVVLTSHSMEECEALCTRMAIMVNGFR RCLGSVOHLKNFGD
GYTIVVRIAGSNPDLKEVQEFFGLAPGSVLKEKHRNMLQYQIPSSLSSILARFSILSS
GSKKRLHIEDYSVSQTTLDQVFVNFAKDQSDDDHLKDLSLHKNJTVVDVAVLTSFLOD
JKQMKKLLKIJKSADRFIJSEGRFWAGLDTKNNVKVWFNNKGWHAJSSFIJNVINNAIL
RANIQKGENPSQYGJTAFNHPLNLTKQQLSEVALMTJSVDVLVSJCVJFAMSFVPASF
                                                                                                                                    ELETNINKLINDTNDTLKSVFLTPPHFCLGRGLIDMVKNQAMADALERFGFNRFVSPLSM
DLVGRNLFAMAVEGVVFFLTTVLJQYRFFTRPRPYKAKLIPDLNIEDEDVRRERQRTLD
GGGNDJLETKELKYRRRRPAVDRTCTGTPPGECFGLJGVNGAGKSTTFKMLTGD
                                                                   VVFL1QERVSKAKHLQF1SGVKPV1YWLSNFVWDMCNYVVPATLVI1IF1CFQQKSYV
                                                                                                   SSTNLPVLALLLLLYGWSITPLMYPASFVFKIPSTAYVVLTSV4LF1GINGSVATFVL
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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhin1; Homin1dae; Homo.
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1 (bases 1 to 44897)
Birren,B., Nusbaum,C. and Lander,E.
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Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
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100.0%; Pred. No. 3.6e-22;
ive 0; Mismatches 0;
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Submitted (30-301-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Gambidge, MA 02141, USA
On Jul 30, 2002 this sequence version replaced gi:17149709.
All repeats were identified using Repeathwisker:
Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@qenome.wi.mit.edu
------- Project Information
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4094: contig of 755 bp in length
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Schome Research
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Aile:,N
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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43337 44060: contig of 724 bp in length
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 11, clone CTD-20280;F. Unpublished
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 59; DB 2;
                                                                    43237 4336: gap of 100 bp
4337 44060: contig of 724 bp
44061 44160: gap of 100 bp
44161 44897: contig of 737 bp
1.ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.0%; Scc...
100.0%; Pred. No. -..
... 0; Mismatches
                                                                                                                                                                                                                                                                                           /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/chromosome-"8"
                                                                                                                                                                                                                                                                                                                                                                                                         /map="8"
/clone="CTD-2319014"
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Matches 59; Conserv
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LOCUS
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JOURNAL
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                               FEATURES
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arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                               sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7956 7904 948 01. 100 bp 7956 7904 948 01. 100 bp 7965 7904 948 01. 100 bp 7965 8603: contig of 699 bp in length 8604 8703; aga of 100 bp 8704 9392 9492; aga of 100 bp 9493 9492; aga of 100 bp 10155: contig of 689 bp in length 10156 10255; gap of 100 bp 10156 10255; gap of 100 bp 10049 1048; aga of 100 bp 10049 11703; gap of 100 bp 11704 11703; gap of 100 bp 11704 11703; gap of 100 bp 11704 11805; contig of 555 bp in length 11704 11805; contig of 701 bp in length 11387; contig of 701 bp in length 11388 11387; contig of 701 bp in length 11388 11388; gap of 100 bp 1388; gap of 100 bp 14688; gap of 100 bp 1468; gap of 1468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1626 2265: contig of 640 bp in length 2266 2365: qap of 100 bp 266 3365: qap of 100 bp 266 3360: contig of 685 bp in length 3151 2015
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3846 3945: gap of 100 bn
3946 3845: gap of 100 bn
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1867: contig of 693 bp in length
187: gap of 100 bp
22680: contig of 713 bp in length
80: qap of 100 bp
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818 1525: contig of 708 bp in length
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1626 2265: contig of 640 bp in length
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of 749 bp in length
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contig of 704 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            717: contig of 717 bp in length
                                                                                                                                                                 * NOTE: This record contains 73 individual
-- Project Information
                                Center project name: L24518
Center clone name: 2028_0_15
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100 bp
if 688 bp in length
100 bp
it 704 bp in length
                                                                                                                                                                                             p of 100 bp contig of 715 bp in length p of 100 bp contig of 713 bp in length
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2272: contig of 706 bp in length
72: qap of 100 bp
33009: contig of 637 bp in length
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693 bp in length
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707 bp in length
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27431: contig of 680 bp in length
                                                                                                                                                100 bp
700 bp in leagth
                                                                                                                                                                                                                                                                                      100 bp
718 bp in length
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34646: contig of 719 bp in length
                                                                                                                                                                                                                                                                                                                                                 length
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37777: contig of 684 bp in length
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712 bp in length
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44144: contig of 681 bp in length
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48884: contig of 687 bp in length
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t 702 bp in 1
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f 695 bp in 1
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29838: contig of 706 bp in
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705 bp in
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649 bp in
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46513: contig of 673 bp in
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704 bp in
                                                                                        713 bp in
                                                                                                                                       701 tsp in
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         6 23595; gap of 100 bp.
24227; contig of 632 bp ir.
24327; gap of 100 bp.
25032; contig of 705 bp ir.
3 25132; gap ot 100 bp.
25838; contig of 706 bp ir.
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187; gap of 100 bp
187; gap of 100 bp
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contig of 701 bp
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40986; contig of
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25838; contig of
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31466: contig of
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40179: contig of
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44939: contig of
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36244: cont.ig of
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45740: cont
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Direct Submission

M. Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire, Submitted (24-SEP-1998) Sanger Centre, Hinxton, Cambridgeshire, Call (28-2) (18-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (28-2) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS931E15 B1874 bp DNA linear PKI 23-NOV-1999 Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence. AL023575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at the Chromosome X http://www.sanger.ac.uk/HGP/ChrX 91815 is from the library MPCTS constructed at the Roswell Park Gancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2 IMPORTANT: This sequence is not the entire insert of clone 931815. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
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The true left end of 424J12 (282207) is at 36643 in this sequence.
The true right end of 506G2 (282213) is at 37431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 39017 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCAGCAGCAGC 38960
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/note="AluSx repeat: matches 292. .1 of consensus" 569. .689.
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                                                                                                                                                                                                                                                                                                 Length 57662:
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52108 52207: gap of 100 bp
52208 52909: contig of 702 bp in length
52910 53009: gap of 100 bp
53010 5365: contig of 656 bp in length
53666 53765: gap of 100 bp
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5366 53765: gap of 100 bp
53766 54444: contig of 679 bp in length
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0
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                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                            Score 58;
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/db_xref-"taxon:9606"
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/clone="RP5-931E15"
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HTG; DXS8098.
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Matches 58; Conserv
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0: 0 . 0 - 0 . 0 . 0 - 0 - 0 .	/note="Alub repeat: matches 2302 of consensus" 5170. 5497 /note="Alub repeat: matches \$6273966 of consensus" 548856445948 /note="Alus repeat: matches 1146 of consensus" 56445948 /note="Alus repeat: matches 1301 of consensus" 59506115 /note="Alus repeat: matches 133290 of consensus" 61566393 /note="Li repeat: matches 39854239 of consensus" 6629677 /note="Li repeat: matches 43774731 of consensus" 6704e="MER2 repeat: matches 195 of consensus" 6704e="MER2 repeat: matches 195 of consensus" 67887073 /note="MER2 repeat: matches 1293 of consensus" 67887575 /note="Alus repeat: matches 1293 of consensus" 6704e="Alus repeat: matches 1293 of consensus" 6704e="Alus repeat: matches 1293 of consensus" 6704e="Li repeat: matches 1293 of consensus" 6704e="Li repeat: matches 1300 of consensus"	e-Alux repeat: matches 1300 of consensus 18815 e-Limbs repeat: matches 47276 of consensus 1.8816 e-Aluxo repeat: matches 2121 of consensus 1.8816 e-Aluxo repeat: matches 2121 of consensus 1.8816 e-Aluxo repeat: matches 2400 of consensus 1.967 e-Aluxo repeat: matches 2400 of consensus 1.967 e-Aluxo repeat: matches 3402 of consensus 1.087 e-Aluxo repeat: matches 1402 of consensus 1.087 e-Aluxo repeat: matches 2400 of consensus 1.088 e-Aluxo repeat: matches 2401 of consensus 1.008 e-Aluxo repeat: matches 2401 of consensus 1.008 e-Aluxo repeat: matches 2401 of consensus 1.008 e-Aluxo repeat: matches 2402 of consensus 1.008 e-Aluxo repeat: matches 2402 of consensus 1.008 e-Aluxo repeat: matches 1.000 of consensus 1.000 e-Aluxo repeat: matches 2402 of consensus 1.000 e-Aluxo repeat: matches 2400 of consensus 1.000 e-Aluxo repeat: matches 2400 of consensus 1.000 e-
repeat_region repeat_region misc_feature repeat_region repeat_region repeat_region	il_region il_region it_region	repeat_region

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14514. 14836

Note-Alubb repeat: matches 13. 302 of consensus"
15126. 15438

Note-Alub repeat: matches 1. 302 of consensus"
15626. 15730

Note-Alub repeat: matches 196. 300 of consensus"
1518. 16420

Note-Alub repeat: matches 196. 300 of consensus"
1618. 16420

Note-Mujb repeat: matches 11. 290 of consensus"
1618. 16420

Note-Flad repeat: matches 117. 6 of consensus"
16120. 1826

Note-Match: STS 124586

Complement(17160. 17224)

Note-Match: STS 124586

Note-Match: STS 124586

Complement(18124. 18827)

Note-Match: STS 124586

Note-Match: STS 124581

Note-Match: STS 12485

Note-Match: STS 12485

Note-STA 12862

Note-STA 12863

Note-
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Anote-"Alusg repeat: matches 1. .296 of consensus"
31359. .31505
Anote-"MER&B repeat: matches 11. .148 of consensus"
32041. .32319
Anote-"Alusx repeat: matches 1. .287 of consensus"
complement(32381. .33599)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(30513, 30706)
/note-"MLT2_internal repeat: matches 4754, 4572 of
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/note-"AluSx repeat: matches 1. 299 of consensus"
31059. 31356
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7060. 33906

7060. 34321

700te "AluJb repeat: matches 1. 301 of consensus"

700te "AluJb repeat: matches 1. 301 of consensus"

complement(34388. 34933)
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Direct Submission

Submitted (02-AGG-2001) Sanger Centre, Binxton, Cambridgeshire, CB10 15A, UK. Email enquiries: humquery@sanger.ac.ik Clone requests: clonerequest@sanger.ac.ik

on Sep 27, 2000 this sequence version replaced quicCt6528.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Fin: EMBL; Swi. SWISSROT; Ti.: TREMHL; Wp., WOMEREP; Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/Clelegans/wolimper Information as sequence is not the entire insert of clone RPI-247C2 It may be also the entire insert of clone RPI-247C2 It may be associate because we sequence overlapping sections only once, except
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regions was finished as follows unless otherwise roted; all regions were either double-strandar or sequenced with an alternate regions were either double-strandar for sequenced with an alternate them stry or covered by high quality data (i.e., phicd quality > 40); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI4 subclone; and the assembly was confirmed by restriction didees. Ref. 247C2 is trom the library RPCI-1 constructed by the group of Pieter de John. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The true left end of clone RP1-247C2 is at 1 in this sequence. The true left end of clone RP5-879JB is at 98251 in this sequence. The
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                                                                                                                                                                                                                                                                                                                                            FRI 03-A0G-2001
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 98360)
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                                                                                                                                                           Db 39890 CIGCCCACCTIGGCCTCCCAAAGTGCTGGGATTACAGGCAIGAGCTGCGCGCCCAGC 39833
                                                                  Saps
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Human DNA sequence from clone RPL 247C2 on chromosome 11pl3
Contains STSs and GSSs, complete sequence.
                                                                                                                     4y 1187 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCCCCAGC
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                                                               Indels
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/note="LiPAll repeat: mutches 2154.
3956, .3992
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2.0%; Score 58; DB 9; L
100.0%; Pred. No. 1.6e-20;
tive 0; Mismatches 0;
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VECTOR: pCYPAC2.
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/db_xref="taxon:9606"
/chromosome="11"
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   Query Match
Best Local Similarity
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586. 8453
/note-"LiPAll repeat: matches 3216. 6162 of consensus*
10697. 10966
/note-"LiMEC repeat: matches 2142. 1979 of consensus*
11202. 11493
/inote-"LiMEC repeat: matches 1978. 2279 of consensus*
13794. 113877
/note-"32 copies 2 mer cc 68% conserved*
14618. 15578
/note-"LTR2 repeat: matches 1. 449 of consensus*
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44071. .44491
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Coter"Charliez repeat: matches 3272, .3370 of consensus"
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4055. - 40840
42053. 42372 repeat: matches 277. 769 of consensus*
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'note-"LiPAll repeat: matches 2215. .3216 o: consensus
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17380. .17654
/note-"MLT1A2 repeat: matches 92. .374 of consensus"
complement(17710. .18372)
/note-"match: GSS: Em:AQ485260"
/note-"match: GSS: Em:AQ545989"
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//note="match: GSS: Em:B04935"
15910. .15911

//note="Single clone region. Assembly confirmed by restriction digest data."
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/note-"13 copies 2 mer tg 92% conserved"
16984. 17077
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Em:AQ488664*
.21177)
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26158)
Em:AQ505438"
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-2610b. .20561
/note-"match: GSS: Em:AZ393320"
29550. .29636
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38585. 38746
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/note="match: GSS:
complement(25626...
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25991. .26104
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL611933 141273 bp DNA linear PRI 11-JUN-2602
Human DNA sequence from clone RPI1-374C13 or clicamosome 1, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regions were either double-stranded or sequenced with an alternate
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Mammalta; Eutherfa; Primates: Catarihin;: Hominidae: Homo.
1 (bases 1 to 141273)
Peck,A.
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18896 g 27671 t.
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  .6144 of consensus'
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                                                                                             /note="LIMD repeat: matches 738, .819 of consensus" 63917, .64021
/note="LIMD repeat: matches 984, .1089 of consensis complement(64074, .64543)
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91625. 191990
//note="THEIC repeat: matches 1. .371 of consensus"
92079. 192337
/note="LIPA7 repeat: matches 5949. .6125 of consens
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63586. 63668
/note-"LIPA2 repeat: matches 900.
63508, .63541
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69990, 70342
                                                                                                                                                                                                       /note-"match: GSS: Em:Au685350"
complement(66096, .66577)
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complement(76460. .76628)
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complement(88581. .89052)
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tive 0; Mismatches
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Description of the state of the
                                                                                                                  was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
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                                                                                                                                                                                                                                    http://www.sanger.ac.uk/HGP/Chrl
RPI1-374Cl3 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
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SWISSPRUT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
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Homo Sapiens chromosome 11, clone RP11-4809, complete sequence.
AC107939
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Birren.H., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RPI1-4809
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a 32122 c 33734 q 40066 t
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/organism-"Homo sapiens"
/db_xref-"taxon:9606"
/chromosome="i"
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A. Sibmitted (16-Nov-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

A. Stonger Thyman, N., Stonger, C., Submission

A. Sibmitted (16-Nov-1999) Whitehead Lostitute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

A. Street, S. 2001, this sequence version replaced gill 443216.

A. Hutp://ftp-genome.washington.edu/HM/RepeatMasker.html
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Homo sapiens clone RP11-21E12, WORKING DRAFT SEGJENCE, 12 unordered
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Mammalia, Eutheria, Primates, Catarilini, Hominidae, Homo.
( bases 1 to 14512)
Birren, B., Linton, L., Nusbaum.C. and Lander.E.
Homo saplens, clone RP11-21E12
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                                                            /rpt_family="Alusq"
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17308. 17574
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                    complement(16631. 16909)
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* NOTE: This is a "working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                      Insert size: 128000; agarose-fp
insert size: 145212; sum-of-contigs
Ouglity coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 8.3 in Q20 bas.
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5758 5857: gap of 100 bp
5658 7545: contig of 1688 bp in length
7546 7645: gap of 100 bp
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                                 Consensus quality: 142529 bases at least Q40 Consensus quality: 144014 bases at least Q30 Consensus quality: 144580 bases at least Q20
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Assembly program: Phrap; version 0.960731
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vector\_side:right"

clone\_end:T7

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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished secuence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC015495 LTG-SEP-2000 Homo Sapiens Clone RP11-21E14, WORKING DRAFT SEQUENCE, 13 unordered
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 155982)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RPII-2IE14
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RefeatMasker.html
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                                                                                                                                                                                                                            QY 1187 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCAACTGCGCCAGG
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Quality coverage: 4.4 in Q2U bases; sum-of-contigs
                                                                                                Length 146312;
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Center clone name: 11_E_14

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big 0ye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 147683 bases at least 040

Consensus quality: 153981 bases at least (220)
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      1112 cthers
                                                                                                                                                                 0; Indels
                                                                                         Ouery Match 2.0%; Score 58; DB 2; Li
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0;
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37592 a 36284 c 35592 g 35732 t
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HTG; HTGS_PHASE1; HTGS_DRAFT
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8186 8285; gap of 100 bp 8286 9661; contig of 8185 bp in length 9622 9761; gap of 100 bp 9762 11131; contig of 1376 bp in length 11132 11231; gap of 100 bp 1123 57431; gap of 100 bp 1123 57436; contig of 46205 bp in length 97437 57536; gap of 100 bp 1132 57437 57536; gap of 100 bp 100 bp
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#1214 92173; contig of 10960 bp in length

92174 92273; qap of 100 bp

92274 103878; contig of 11605 bp in length

103879 103978; gap of 100 bp

103979 120091; contig of 16113 bp in length
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61395: contig of 3859 bp in length
495: gap of 100 bp
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71509: contig of 5795 bp in length
609: gap of 100 bp
81113: contig of 9504 bp in length
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Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 58; Conservative 0; Mismatches 0;
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120192, 154009
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154110, .155982
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/note="assembly_fragment"
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/hote="assembly_fragment"
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103979, ,120091
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Streng B. Lincon... Nusbaum.C., Lander,E., Abraham.B., Allen,N., Anderson,S., Baldwin,J., Barana,N., Beckerly,R., Heda.F., Anderson,S., Baldwin,J., Barana,N., Beckerly,R., Heda.F., Castle,A., Choepel,T., Colargelo,M., Collins,S., Collymore,A., Coske,P., Dearellano,K., Dewis,K., Doyle,M., Ferester,J., Perester, M., Ferester,J., Cartia,P., Fitzhugh,W., Forrest,C., Gage,D., Galagan,J., Gardraga,K., Mannaon,R., Jones,C., Kann, M., Morton,L., Howland,J.C., Johnson,R., Jones,C., Kann, M., Mischard, M., Merenan,K., Madodnad,J.C., Johnson,R., Jones,C., Kann,C., Liu,G., Jones, M., Merenan,R., Madodnad,P., Marquis,N., Metwar,P., McGark,A., McKennan,R., Moldrim,J., Meneus,L., Mortow,J., Nayjer,J., Norman,C.H., O'Connor,T., O'Donnell,P., Gilvar,T.M., Deterson,R., Pleari,C., Pollara,V., Raymond,C., Riley,K., Rottman,C., Suntos,R., Santos,R., Talamas,J., Testaye,S., Theodore,J., Threel,A., And Sashilas,A., Talamas,J., Testaye,S., Theodore,J., Threel,A., And M., Massillas,M., Talamas,J., Testaye,S., Theodore,J., Threel,A., And M., Massillas,M., Viel,R., Vo,A., Wax,N., Wyman,D., Ye,W.S., Zimmer,A.
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Birren.B., Linton.L., Nusbaum,C., Lander.E., Ali A., Allen.N., Anderson.S., Barna,N., Bastleir.V., Bloom,T., Mey. Slavkiy,L., Boukhqaiter.B., Brown,A., Comarata.D., Compoplanc.A., Charg.J., Characo.B., Choepel.Y., Colangelo.M., Colling.S., Forley.B., FirzGerall.M., FirzGerall.M., FirzGerall.M., Galden.B., Bodge.S., Farreira,P., FirzGerall.M., FirzGerib.M., Gaste.D., Gardqan.S., Gardqan.S., Ginde.S., Gold.S., Goyetter.M., Graham,D., Galdqan.J., Garddyn.S., Ginde.S., Gold.S., Goyetter.M., Craham,D., Candrib.M., MacGerall.M., FirzGerib.M., MacGerall.M., FirzGerib.M., MacGerib.M., MacGerib.M., MacGerib.M., MacGerib.M., MacGerib.M., Major.J., Marquis.M., Luck.L., Lakerie.M., MacCol.M., MacGerib.M., Major.J., Marquis.M., MacGerib.M., Major.J., Marquis.M., MacGerib.M., MacGerib.M., Major.J., Marquis.M., MacGerib.M., Major.J., Marquis.M., Mihova.T., Mihova.T., MicGerib.M., Major.J., Marga.M., Mihova.T., MacGerib.M., Major.J., Marga.M., Mihova.T., MacGerib.M., Major.J., Marga.M., Mihova.T., MacGerib.M., Major.M., Mihova.T., MacGerib.M., Major.M., Mihova.T., Marga.M., Santos.M., Santos.M., Santos.M., Stolaner.S., Santos.M., Stolaner.S., Santos.M., Stolaner.S., Santos.M., Stolaner.S., Santos.M., Stolaner.S., Santos.M., Milson.B., Wall.M., Wall.M., Wall.M., Wall.M., Wall.M., Wall.M., Wall.M., Wall.M., Wall.M., Wall.D., Young.G., Zambek.L., Zammer.A. and Zody,R., MacGerib.M., Wall.M., Mall.M., Wall.M., Wall.M., Wall.M., Mall.M., Mall.M., Mall.M., Wall.M., 
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 15 cione Reli 233Cii mag. 15, *** SEQUENCING
IN PROGRESS ***, 2 ordered pieces.
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Research, 320 Charles Street, Cambridge, NA 0414. USA
On Jun 1, 2002 this Sequence version replaced of 20-4464.
All repeats were identified using RepeatMasker:
Smit. A.F.A. & Green, P. (1996-1997)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 158071)
HTG: HTGS_PHASE2: HTGS_FULLTOP: HTGS_ACTIVEFIN
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Surren, B. Linton, L. Nusbaum, C., Lander, E., Abraham, H., Ailen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Bodwila, S., Bodwila, R., Brown, A., Burkett, G., Calmpopiano, A., Castle, A., Choepel, Y., Colangolo, M., Collins, S., Collymore, A., Cooke, P., Learellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhuji, W., Gaqe, D., Galdquin, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakoquo, K., Lamaezeres, R., Landers, T., Lehoczky, J., Revine, R., Live, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McTartly, M., McFwan, P., McGurk, A., McKernan, K., Mergay, V., Morrow, J., Murchy, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nori, J., Liver, J., Norman, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Folllara, V., Raymond, C., Kiley, R., Rogov, P., Rothman, D., Pisani, C., Folllara, V., Raymond, C., Kiley, R., Rogov, P., Rothman, D.,
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Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                      consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is telleved to be currect as given, however the sizes of the daps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by the finished sequence as soon as it is available and the accession number will be preserved.

4.1244: contig of 41244 bp in length
41245 41344: gap of 100 bp
41345 158071: contig of 116727 bp in length.
                                                                                                                                                                                                                                                           * NOTE: This is a 'working draft' sequence. It currently
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100.0%; Pred. No. 1.7e-20;
                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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                              Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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Matches 58; Conservative 0; Mismatches
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1. 158071
Augustens-Momo sapiens-
/db xref-"taxon:9606"
/chromosome-"15"
                                                                                                                                                                                                                                                                                                                                                                                                                   provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                             clone name: 233_C_13
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19929 16928: gap of 100 bp 19929 121274: contig of 12246 bp in length 121275 121774: qap of 100 bp 121375 141287: contig of 19913 bp in length 121378 141387: gap of 100 bp 141388 158450: contig of 17063 bp in length Location/Qualifiers
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85928 96327: contig of 10400 bp in length
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           76899 76998: gap of 100 bp
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68457. .76898
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121375. 141287
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27753. .31395
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23844. .27652
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Roy.A., Santos,R., Schauer,S., Severy,P., Spender,H., Stange-Thomann.N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo.A., Wilson,H., Wu,X., Myman,D., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

1. Submitted (28 ARR-2000) Whitehead institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 4, 2000 this sequence version teplaced at 76.8356.

All repeats were identified using RepeatMasker:
Smit, A.K. & Green, P. (1996, 1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence, It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence :ceard is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 3.6 in 020 bases; agarose-1p
Quality coverage: 3.8 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: M3: M77815: 100% of reads
Sequencing vector: M3: M77815: 100% of reads
Chemistry: Dye-terminator Bid (bye: 100% of reads
Assembly program: Phrap: version 0.96073:
Consensus quality: 146955 bases at least 040
Consensus quality: 151080 bases at least 020
Consensus quality: 155108 bases at least 020
Insert size: 155000: agarose-fp
Insert size: 155050; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                               3170 3269; gap of 100 kp 4574 4673; contig of 1304 kp in length 4574 4673; gap of 100 kp 100 kp 7998 8097; gap of 100 kp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1750 1849: gap of 100 bp
1850 3169: contig of 1320 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 3993 bp in length
5 of 100 bp
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95; gap of 100 bp
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47307: contig of 4942 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1749: contiq of 1749 by in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43: gap of 100 bp
27652: contig of 3809 bp in length
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76898: contig of 8442 hp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1345; gap of 100 bp.
16766; contra of 4621 bp. in.
16766; contra of 4621 bp. in.
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                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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52438: con
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42266
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60136
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68457
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BASE COUNT
ORIGIN
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JOURNAL
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AC019307
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                                                                                                                                                                                                                    AC093737 162419 bp UNA Linear ETS 10-SEP-2001
Homo sapiens chromosome 2 clone RPI1-21M2. WCRKIN: URAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Symptod (10-SEP-2001) Genome Sequencing Center, washington
University School of Medicine, 4444 Forest Park Parksay, St. Louis,
Mc 63108, USA
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Primates, Catarriini, Hominidue, Homo. 1 (bases 1 to 162419) Waterston, R.H.
                                                                                  Saps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
        Length 15845F;
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Sequencing vector: plasmid; 64%
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator Bit Dye; 100% of reads
Assembly program: Phrap; version 0.990019
Consensus quality: 162004 bases at least 249
Consensus quality: 16215 bases at least 249
Consensus quality: 162211 bases at least 249
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HTG: HTGS_PHASE1; HTGS_PRAFT; HTGS_FULLIOP
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            DB 2; Le
1.7e-20;
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                    100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence of Homo sapiens cloue Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism-"Homo saplens"
            Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref-"taxon:9606"
/chromosome-"2"
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1. 162419
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vector_side:right"
70351. .162419
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Waterston, R.H.
                                                                                                                                                                                                                                                              2 unordered pieces.
Guery Match
Best Local Similarity 100.0
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Homo sapiens
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KEYWORDS
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R Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Coloepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, F.,

Boguslavkiy, Bornar, G., Bomino, M., Doyle, M., Fenestor, J.,

Ferreira, F., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,

Forreira, F., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,

Rowland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Kieln, J.,

Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

McCdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,

McCheeters, R., Maldrim, J., McDann, P., McGurk, A., McKernan, K.,

McCheeters, R., Maldrim, J., Woenels, L., Morrow, J., Naylor, J.,

Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,

Pitrell, A., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Ilrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wynan, D., Ye, W. J.,

Zimmer, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wynan, D., Ye, W. J.,

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Zimmer, A. and Zody, M., Viel, R., Vo, A., Wu, X., Wynan, D., Ye, W. J.,

Zimmer, A. and Zody, M., Viel, R., 
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Mono sapiens chromosome 8 clone RPII-359Pil map 8, WORKING DRAFT
SEQUENCE, 33 unordered pieces.
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        by
        1187
        CTGCCCCCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC
        1244

        by
        52046
        CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCAGC
        52103

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1 (bases 1 to 166011)
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                                                                                                                                                                                                                                                                            Length 162419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                   100 others
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Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RPII-359PII Unpublished
                                                                                                                                                                                                                                                                  2.0%; Score 58; DB 2; L
100.0%; Pred. No. 1.7e-20;
Live 0; Mismatches 0;
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Web site: http://www-seq.wi.mit.edu
/note-"assembly_name:Contig14 clone_end:SP6
                                                                                    vector_side:right"
| 30933 c 30950 q 50417 t
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AC019307.3 GI:7249157
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Best Local Similarity 100.0%
Matches 58; Conservative
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Homo sapiens
                                                                                                                                   50019 a
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Query Match
                                              NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the Fieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Quality coverage: 3.9 in Q20 bases, agarose-tp Quality coverage: 4.3 in Q20 bases, sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8715: gap of 100 kp
120908: contig of 12193 bp in length
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120909 121008; gap of 100 bp
121009 131478; contig of 10470 bp in length
131479 131578; gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14184: gap of 100 bp
15991: contig of 1807 bp in length
16091: gap of 100 bp
18891: contig of 2800 bp in length
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contig of 6448 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98885: gap of 100 kp
108615: contiq of 9730 bp in length
                                                                                                                                                                                         1 1042; contig o: 1042 bp in :enath
1043 1142; qap of 100 bp
1143 2242; contig of 1000 bp in lenath
2143 2242; contig of 1000 bp in lenath
3711 3810; qap of 100 bp
                                                                                                                                                                                                                                                                                                                   5157: gap of 100 bp 6697: contig of 1540 bp in length 7389: contig of 592 bp in length 7489: gap of 100 bp 100 bp 8708: contig of 1219 bp in length 6708: contig of 1219 bp in length
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38: contig of 1462 bp in length
gap of 100 bp
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72618: contig of 7935 up in length
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85048: contig of 65±2 bp in length
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10176: contig of 1168 bp in length
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contig of 2544 bp is length
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37294: contiq of 4453 kp in
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5 of 100 bp
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23808: cont.
23908: gap of
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42230: con
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11738: con
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131579 144478: gap of 12800 bp in length 144379 144478: gap of 100 bp 144479 166011: contig of 21533 bp in length. Location/Qualifiers
                                                                                                                                                /clone_lib-"RPCI-11 Human Male BAC"
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18992. 21414
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751515. 23808
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8735. 42230
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91697. .98785
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28164. .32741
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                                                                                                                                 /clone-*RP11-359P11*
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25520, .28063
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                                               FEATURES
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Length 166011;

2.0%; Score 58; DB 2;

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Center code: WUGSC
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KEYWORDS
SOURCE
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Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boyuslawity, L., Boukhadater, B., Brown, A., Burkett, G.,
Campop, ano, A., Castle, A., Choppel, Y., Colange, G.M., Cellins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Caldgan, J., Gardya, S., Ginde, S., Goyette, M., Gate, D.,
Grand-Pierre, N., Grant, G., Hagos, B., Heatord, A., Herton, C.,
Howland, J., LaRocque, K., Johnes, C., Karn, C., Karn, C.,
Klein, J., LaRocque, K., Johnes, C., Karn, C., Karn, C.,
Howland, J., LaRocque, K., Johnes, C., Marguis, M.,
Murphy, T., Law, C., Liu, G., Locke, K., Macdon, J.P., Marguis, M.,
Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, T., O'Connor, T.,
Pisan, C., Pollara, V., Raymond, C., Ritey, R., Rothman, D.,
Pisan, C., Pollara, V., Raymond, C., Ritey, R., Rothman, D.,
Stange-Thomann, N., Schauer, S., Severy, P., Spencer, R.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigilio, J.,
Voung, G., Zahnoun, J., Zimmer, A., dilson, R., Wuman, D., Ye, W. J.,
Voung, G., Zahnoun, J., Zimmer, A., dilson, R., Wuman, D., Ye, W. J.,
Chhairted, J., Sanko, S., Sanko, M., K., Nyman, D., Ye, W. J.,
Voung, G., Zahnoun, J., Zimmer, A., dilson, R., Wuman, D., Ye, W. J.,
Chemitted, J., Subrassion
                                                                                                                                                                                                                                                                                                                      AC069120 177533 bp DNA linear HTG 15-NOV-2001
Homo saptens chromosome 8 clone RP11-675F6 map 8, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
                               Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. [ (bases 1 to 177533) Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 8, clone RP1]-675F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18 MAY-2000) Whitehead fast tote/MJI Center for Getome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 15, 2001 this sequence version replaced girl3357522.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ M:T Center for Genome Research
                                                                                                                                  DD 51640 CTGCCCACCTTGCCTCCCAAAGTGCTGGGATTACAGGATGAGGATGAGGACCTGCAGC 51697
                                                                                                  1187 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCGACTGAGTCAGC 1244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      All repeats were identified using RepeatMasker:
Smit, A.F.A. 6 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1254 1353: gap of 100 bp
1354 26734: contiq of 25381 bp in length
                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Pred. No. 1.7e-20;
; Mismatches 0;
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Host Local Similarity 100.0%; P
Matches 58; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC069120.4 GI:16931029
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LOCUS
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JOURNAL
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AUTHORS
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SOURCE
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COMMENT

TITLE

VERSION

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Homo sapiens chromosome 15 clone RPII-528N4, WORKING DRAFT SECTIONS ACOLIVE, 12 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 188820)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 1187 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCAGG
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                                                                                                                                            191500 108700: qap of 100 bp 108701 114249: contig of 5549 bp in length 114250 114349: gap of 100 bp 114350 126608: contig of 12459 bp in length 126809 126808: contig of 12459 bp in length 126809 137847: contig of 109 bp 137848 137947: qap of 100 bp 140144 140243: qap of 100 bp 140144 140243: qap of 100 bp 140144 140243: qap of 100 bp 143410 145669: contig of 2260 bp in length 143410 145669: contig of 2260 bp in length 145670 145769: qap of 100 bp 145670 14569: contig of 2885 bp in length 145770 154564: contig of 3885 bp in length 145770 154154: contig of 3885 bp in length 145770 154154: contig of 3885 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib-"RPCI-11 Human Male BAC"
a 40970 c 39158 g 49339 t 1505 others
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                                   91265: contig of 30504 bp in length
                                                                                                      365: qap of 100 bp
108600: contig of 17235 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 11156 bp in length.
134: gap of 100 bp
60661: contig of 33827 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154155 154254: qap of 100 bp
154255 15634: contig of 2180 bp in length
156435 156374: qap of 100 bp
156535 166277: contig of 9743 bp in length
166278 166377: qap of 100 bp
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1.7e~20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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177533: cont.i
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AC013281.5 GI:10048071
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.0%;
Best Local Similarity 100.0%;
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                                                       60662 60751:
                                                                                                      91266 91365:
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166378 1775
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**NOTE: This is a 'working draft' sequence. It currently consists of 12 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                          Insert size: 203000; agarose-fp
Insert size: 189063; sum-or-contigs
Quality coverage: 4 28 in 020 bases; agarose-fp
Quality coverage: 4.60 in 020 bases; sum-or-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 3024 hp in length contig of 3024 hp in length gap of unknown length contig of 6524 bp in length gap of unknown length contig of 10480 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 13207 bp in contig of 13712 bp in contig of 13712 bp in contig of 13712 bp in contig of unknown length contig of 14161 bp in length contig of unknown length
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Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2415: contig of 2415 bp in length
                                                                                                                 Chemistry: Dye-primer El: 76% of reads
Chemistry: Dye-terminator Big Dye: 24% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179527 bases at least C40
Consensus quality: 182913 bases at least C40
Consensus quality: 184575 bases at least C20
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62224. .75585
/note-"assembly_name:Costigl?"
75686. .90351
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/note="assembly_name:Contig6"
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/note-"assembly_name:Cont.q8"
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clone_end:SP6
                                                        --- Summary Statistics
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/db_xref-"taxon:9606"
/chromosome-"15"
                                       Center project name: H_NH0528N04
                                                                                                   Sequencing vector: plasmid: 24%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .188820
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36151. .47862
                                                                              Sequencing vector: M13; 76%
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5539:
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12263:
22743:
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PRI 09-JAN-2002
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Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missour: 63108, USA 0.010 Jul 3, 2001 this sequence version replaced 91:13411202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (02-R/W-1999) Genome Sequencing Center, Mashington
Diversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63109, USA
4 (bases 1 to 192396)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammallai Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19239)
Sulston, J. E. and Materston, R.
                                                                                                                                                                                                                                                                                                                                    Db 123691 CTGCCCACCTTGGCCTCCCAAACTGCTGGGATTACAGGCATGAGCCACTGGGCCCCAGC 123748
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Homo sapiens BAC clone RP11-458D8 from 2, complete sequence.
AC012668
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                                                                                                                                                                                                                          2.0%; Score 58; DB 2; Length 18882C;
100.0%; Pred. No. 1.7e-20;
                                                                                                                                                        1107 others
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Waligorski,J., Cotton,M. and Elliott,G.
The Sequence of Homo sapiens BAC clone RP11-458D8
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Web site: http://genome.wustl.edu/gsc
Conlact: sapiens@watson.wustl.edu
/note-"assembly_name:Contigl3"
90452. 110259
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110360. .140334
/note-"assembly_name:Contigl5"
140435. .180820
/note-"assembly_name:Contigl6"
a 45259 c 44833 g 48717 t 110
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Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.
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3 (bases 1 to 192396)
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Best Local Similarity 100.0
Matches 58; Conservative
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3258, .13442
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10680. .10824
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2875. .13046
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7599. .17947
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7577. .17598
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20001. .20295
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6351, 16624
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(bitp://bacpac.med.buffalo.edu)
                                                                                                                                              Mapping information for this close was provided by a lebt b. Appring the Person Department of Genetics, Washington University, St. Loris MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., paned quality >- 0); an attempt was made to resolve all sequenting problems, such as compressions and repeats; all regions were rowered by sequence from more than one subclone; and the assembly was continued by
                                                                                                                                                                                                                                                                                                                                                                                                                                 The clone sequenced to the left is RPII-556F21. 2003 bp overlap; the clone sequenced to the right is RPII-489F15. Actual start of this clone is at base position 1 of RPII-456D8; actual end is at base position 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Data from 97986 to 98116 is covered only by a single plasmid subclone. Data from H_AC012462 was used to finish this clone, AC012668,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xret-"taxon:9606"
/chromosome."2"
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2562. 2842
/rpt_family *L1"
2843. 29.7
/rpt_family *L1"
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/rpt_family="MER2_type"
2154, .2319
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1182. .1221
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1. .192396
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5349, 6247
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4157. .4188
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4977, 5050
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6007. .6027
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193314 bp DNA Linear RTG 21-JCL-2091

Bomo sapiens chromosome 15 clone RP11-528N4 map 15, WCKKING DRAFT

SEQUENCE, 13 unordered pieces.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
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Submitted (05-JAN-2001) Whitehead Institute/MII Seater for Senome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 20, 2001 this sequence version repraced qiil4389345.
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                                                                                                                     Length 192396;
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker htm.
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Sequencing vector: Plasmid: n/s. 100% or reads
Chemistry: Dye-terminator Big 1990: 100% of reads
Assembly program: Phrap: version 0.960731
Consensus quality: 19974 hases at least u40
Consensus quality: 191073 bases at least u40
Consensus quality: 191547 bases at least u20
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                                                                                                                                                                                     0; Mismatches
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100.0%; Pred. No.
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                                        /rpt_family="MIR"
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22418. .22570
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Matches 58; Conservative
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TITLE
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arbittary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                        NOIE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
Insert size: 192114; sum-of-contigs
Quality coverage: 10.4 in Q20 bases; agarose-fp
Quality coverage: 10.2 in Q20 bases; sum-of-contigs
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18868+ 193314: contig of 34632 bp in length.
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69296: contig of 11178 bp in length
396: gap of 100 bp
81566: contig of 12170 bp in length
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111826: contig of 19381 bp in length
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28798 29674: contig of 877 bp in length
29675 29774: gap of 100 bp
29775 32294: contig of 2520 bp in length
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/organism-"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                       HSBA425M5 194433 bp DNA linea: FRI 14-MAK-2001 Human DNA sequence from clone RPI1-425M5 on chromosome 20 Contains a GLRX (glutaredoxin (thiolitranslerase)) pseudogene, a PPIA (peptidylprolyl isomerase A (cyclopiilin A)) pseudosene, the NNAT gene for neuronatin, the BLCAP gene for bladder cancer 10 kD protein BCI0, a purative novel transcript, ESIS, SISS, GSSS and ALI09614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-MAR-2001) Sanger Sentre, Hinxton, Cambidgeshire, CB10 15A, UK. E-mail enquiries: humquery%sanger.ac.uk Gione requests: clonerequest&sanger.ac.uk clonerequest&sanger.ac.uk clone of the sequence version replaced qi:7329727.

On Jun 26, 2000 this sequence version replaced qi:7329727.

Mirror differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we sutmit sequences with only a small overlap as described above.
                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The following abbreviations are used to associate primary accession unibers given in the feature table with their solitee databases:
Emily EMBLS SW1, SW1SSPCT; TILL TERMEL, WP.: WHMPET Information on the WORMPEP database can be trunk at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence is the entire inserf of clume RELL-425M5 The true left end of clone RP4-640H8 is at 1761B7 in this sequence. The true right end of clone RP4-592G19 is at 59744 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least assembly was confirmed by restriction digest. Spil-425M5 is from the library RPCT-11.2 constructed by the group of Pieter de Joeq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/f elegans/w.rmpcp This sequence was generated from part of bacterial clone centius of human elemonsome 20, constructed by the Sanaer feature Circhnosome 20 Mapping Group. Further information can be toled at http://www.sanger.ac.uk/HGP/Chr20
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL109614.28 GI:8745190
HTG: BC10; BLCAP: CpG island; cyclophilin; GLKX; neuronatin; NNAT
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                   QY 1187 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGGATGAGGCACTGCGGCAGG 1244
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                                                                                                                      2.0%; Score 58; DB 2; Length 19344;
                                            1204 others
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                                                                                                                                              1.7e-20;
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51569 a 46564 c 45000 g 48977 t.
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VECTOR: pBACe3.6
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/db_xref="taxon:9606"
                                                                                                                                                 Pred. No.
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Mammalia; Eutheria; Primates;
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/clone="RP11-425M5"
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Phillimore, B.
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clone_end:T7
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58;
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DEFINITION
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TITLE
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2375. .2513
/note="AluSg/x repeat: matches 175. .308 of consensus"
2516. .2541
/note="U2_repeat: matches 5. .33 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                   274] 3206 ---- matches 5283, 5748 or consensus"
/note="LIME2 repeat: matches 5283, 5748 or consensus"
3207 3525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8053. 8364

/noth-Aludo repeat: matches 1. 302 of consensus"

7100.e-"LIME3 repeat: matches 5545. 5755 of consensus"
                                                                                                                                                                                                                                                                     'note-"LIME2 repeat: matches 5746. .6163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7292. .8014
/cote-"LIMEl repeat: matches 5444. .6163 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5283 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-*LIM4 repeat: matches 4669. .4987 of consensus* 3857. .4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"LIM4 repeat: matches 4541. .4669 of consensus"
4521. .4624
/note-"MIR repeat: matches 47. .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o/62. ./013
/note="LTR16C repeat: matches 133. .387 of ronsensus"
                                                                   matches 3. .80 of consensus"
                                                                                                                                                                               /note="MLT1F repeat: matches 170. .540 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note-"MLTIC repeat: matches 129. .466 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-*L2 repeat: matches 581. .713 of consensus* 5623. .5850
note-*L2 repeat: matches 1312. .1557 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9165. .9444
/note="AluJo repeat: matches 40, .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .2 repeat: matches 2649. .2710 of consensus ^{*} 0_{13}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9706. .10153
/note-"L2 repeat: matches 1057. .1554 of consensus*
10598. .10799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mote-"L2 repeat: matches 2111, .2358 of consensus" 0862, .10958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // // MLTIC repeat: matches 98. .129 of consensus 11299. .11721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12065. 1241.
7001e-12 repeat: matches 2389. .2706 of consensus.
13039. .13353
                                                                                                                                                                                                         1528. .1827
//botc.-*Alusx repeat: matches 1. .299 of consensus"
1560. .2374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alusq repeat: matches 1. .201 of consensus" 2741. .4206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3207. 3525
/note="AluJb repeat: matches 1. 303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5861. 6031
/note-*FRAM repeat: matches 1312. 1557 of consensu:
6420. 6487
/note-*L2 repeat: matches 54.0
6762. 7013
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11267. .11298
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                                                                                                           /note-"MLT1-INTERNAL repeat: matches 308. .583 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"MSTA repeat: matches 1. .426 of consensus"
11722. .12061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3526. 3551
/note-*LIME2 repeat: matches 5258.
3539. 3856
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/note-"LiME3 repeat: matches 5763,
9165. 9444
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14310. .14793
                                                    /note-"AluJ/FLAM repeat:
/clone_lib-"RPCI-11.2"
9. .R6
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/note=*L2 re
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n 24667, 24947.

n 24667, 24947.

n 25177, 25257

n 25177, 25275

n 25177, 25275

n 25136, 25689

n 25336, 25689

n 2536, 25689

n 2560, 25689

n 2560, 25689

n 25700, 26011

n 25700, 26011

n 25701, 26841

n 26012, 26841

n 26012, 26841

n 26012, 26841

n 26012, 26841

n 27796

n 2751, 2751 of consensus

complement(27254, 27711)

n 2751, 27796

n 2751, 28088

n 2757, 28088

n 2757, 28088

n 2757, 28088

n 2602, 28088

n 2757, 28088

n 28089, 28720

n 28720

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//note="march: GSS: Em:AQU59989"

21158. .2123

//note="L2 repeat: matches 2066..2119 of consensus"

21214. .21538

//note="Musx repeat: matches 1..312 of consensus"

21539. .22081

//note="L2 repeat: matches 2119..2792 of consensus"

22089. .22510

//note="L2 repeat: matches 1148..1567 of consensus"

//note="L2 repeat: matches 1148..1567 of consensus"
                                                                                                                                                                                                             16314, 16444
/note="L2 repeat: matches 2092, .222] of Cinsensus 16445, .16851
/note="L1M4 repeat: matches 5014, .540, of Consensus" 1656, .1762
/note="L2 repeat: matches 2174 .2380 of Consensus" 17802, .17852
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/note="LIM4 repeat: matches 4532, .4854 of consensus"
23624, .23826
23624, .23826
24119, .24589
/note="Inality consensus"
24025, .2450
/note="23 copies 2 mer tt 78% conserved"
24271, .24576
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"LIME repeat: matches 5394, .5808 of consensus"
18164, .18298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5012 of consensus
                                                                                                                  /note="12 repeat: matches 2692, .2745 of consensus"
15598, .1611
//note="12 repeat: matches ill9, .2029 of consensus"
16314, .16444
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/note="L2 repeat: matches 2593, .2687 of consensus"
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29381. .29418
//note="12 repeat: matches 2556. .2593 of consensus"
29419. .29747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .307 of consensus"
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                                                                .244 of consensus"
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29748, .29842
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/note="match: GSS: Em:AQ812308"
15382. .15581
                                                  /note-"MIR repeat: matches 39.
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Length 194433;

2.0%; Score 58; DB 9; L 100.0%; Pred. No. 1.7e-20;

Query Match Best Local Similarity

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ALAUS961 195386 bp DNA linear HIG 09-AUG-2002 Homo sapiers chromosome l clone RP11-718D19, *** SEQUENCING IN PROCRESS ***, in ordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 195386)
Van Hellmond,Z.
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Submitted (31-30L-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Chone requests: chonerequest@sanger.ac.uk
On Aug 11, 2002 this sequence version replaced gi:22003315.
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Contact: http://www.sunger.ac.uk
Center project name: bA718D19
Consembly program: bA78B19
Chamistry: Dye-terminator; 100% of reads
Consensus quality: 195348 bases at least Q40
Consensus quality: 195366 bases at least Q20
Consensus quality: 195366 bases at least Q20
Inscrt. size: 185386: sum-of-contigs
Inscrt. size: 18132; 9-2% error: agarise-fp
Quality coverage: 12.0% in Q20 bases; sum-of-contigs Quality
coverage: 13.15x in Q20 bases; agarose-fp
                                                                          Db 148147 CIGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCAGC 148090
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Gaps
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HTG: HIGS_PHASE2: HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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48905 a 47558 c 50028 g 48895 t
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Web site: http://www.sanger.ac.uk
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/db_xref-"taxon:9606"
/chromosome-"l"
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KEYWORDS
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8643 58742; gap of unknown length 67478; contig of 8736 bp in length 67578; gap of unknown length 7479 6865; contig of 11087 bp in length 8666 88765; contig of 11087 bp in length 8766 88765; contig of 1967 bp in length 8768 8862; gap of unknown length 8863 99534; contig of 10572 bp in length 9873 8862; gap of unknown length 9973; gap of unknown length 9973; 109972; contig of 10572 bp in length 9973 109972; gap of unknown length 109972; contig of 18016 bp in length 9873 109973; gap of unknown length 109973; gap 
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1362. 17096
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17197. 21173
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/note-"assembly_name:Contig25"
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37685. 44969
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/organism-"Homo sapiens"
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                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 196520)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                   Nov 17, 2000 this sequence version replaced gi:11034995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector; plasmid: 0% of reads Chemistry: Dye-primer ET; 100% of reads Chemistry: Dye-primer ET; 100% of reads Assembly program: Phrap; version 6.990319 Consensus quality: 180026 bases at least Q40 Consensus quality: 180505 bases at least Q40 Consensus quality: 180505 bases at least Q40 Consensus quality: 180507 bases at least Q20 consensus quality: 180507 squicker pp Insert size: 193909; agarose fp Insert size: 193909; agarose fp Unality coverage: 4.17 in Q20 bases; sum-of-contist Q20 bases; sum-of-contists
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contig of 1063 bp in Jenath
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contig of 1061 bp in Length
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2 (bases 1 to 196520)
Walerston, R.H.
SEQUENCE, 27 unordered pieces
                                   ACO83830.3 GI:11192238
HTG: HTGS_PHASE1; HTGS_DRAFT
HOMO Sapiens.
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* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                            4155 4254: gap of 100 pp
4255 18703: contig of 14449 bp in length
18704 18803: gap of 100 bp
18804 20941: contig of 2138 bp in length
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176337 187128: contig of 10792 bp in length
187129 187228: qap of 100 bp
187229 190959: qap of 135 bp
190960 201197: contig of 10238 bp in length
                                                                                                                                                                                                                    20542 21041: gap of 100 bp
21042 34907: contig of 13866 bp in length
34508 35012: gap of 105 bp
35013 37508: contig of 2496 bp in length
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93487 123956; contig of 33470 bp in length
123957 124056; gap of 100 bp
124057 147917; contig of 23861 bp in length
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176236: contig of 28219 bp in length
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52840 56933: contlq of 4094 bp in length
56934 57033: gap of 100 bp
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37609. 52739
/wote-*assembly_fragment:00671.0*
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Znote="assembly_fragment:01287.0"
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/note-"assembly_tragment:02486
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/note-"assembly_tragment:04764
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/note-"assembly_tragment.04816"
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fragment_chain:2"
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//note-"assembly, fragment:03624
fragment.chain:2"
85008. .37508
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1. .201197
/organism-"Homo sapiens"
/db_xief-"taxon:9606"
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/clone="KP3-424312"
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Mammalia: Eutheria; Primates: Catarrhini: Hambidae: Homo.
1 (bases 1 to 201197)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Standited (09-JUL-2001) Sanger Frentze, Hildrein, Candinddeshire,
CBIO 1SA, UK. E-mail enquities: Nummy artydsanatrianiuk CLine
requests: Clonerequest@sanger.ai uk
CD Jan 22, 2001 this sequence version replaced quality (00 Jan 22, 2001 this sequence version replaced quality).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Guery Match 2.0%; Score 58; DB 2; Length 196520; Best Local Similarity 100.0%; Pred. No. 1.7e-20; Matches 58; Conservative 0; Mismatches 0; Indels 3
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Quality coverage: 6.87x in Q20 bases, summon contast
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Assembly program: XGRP4; version 4.5
Sequencing vector: M13; M77815; 74% of reads
Sequencing vector: M13; M77815; 74% of reads
Chemistry: Dye-terminator B14 Bye; 4% of reads
Chemistry: Dye-terminator AB1; y6% of reads
Chemistry: Dye-primer amerisham; 2% of reads
Chemistry: Dye-primer amerisham; 2% of reads
Chemistry: Dye-primer B19 Bye; 6% of reads
Consensus quality: 19431 bases at least
Consensus quality: 196512 bases at least Occ
Consensus quality: 196512 bases at least Occ
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                                                     125089, 138218
7note-*assembly_name:Contid38"
138319, 156668
7note-*assembly_name:Contig39"
156769, 175115
                                                                                                                                                                                                                                                                                                                       67579, 78665
/note-"assembly_name:Contid33"
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/note-"assembly_name:Contiq32"
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Web site: http://www.sanger.ac..x
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Stange-Thomann, N., Stojanovic, N., Talamas, J.,

Genome Center

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Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,K., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                Submitted (19-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 19, 2002 this sequence version replaced g1:22213416. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conter: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
...... Project information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
                                                                                                                                                    Direct Submission
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*** SEQUENCING
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 29270)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy 1187 CIGCCCACTTGGCCTCCCAAAGTGCTGGGATTACAGGATGAGGACTGGACTCAGGC 1244
Db 60280 CIGCCCACTTGGCCTCCCAAAGTGCTGGATTACAGGCATGAGCACTGGGCCCAGC E 223
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55207 a 43266 c 43712 q 57504 t. 1508 c*hers
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   /note-"assembly_frayment:05572.0"
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/note="assembly_fragment:03867
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                * arbitlary, Gaps between the contigs are represented as renns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suzaki, D., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
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Homo sapiens cDNA FLJ37503 tis, clone BRAWH2016679.
AK094822
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140072 151044: contig of 10973 bp in length
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Homo sapiens brain cDNA to mRNA, clone_lib:BRAWH2
clone:BKAWH2016679.
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/close_lib="RPC1-11 Human Male BAC"
83142 d 66391 c 66021 g 76579 t 570
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Center project name: L6996
Center clone name: 493_E_3
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/chromosome+"20"
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151145 17956: conti
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179757 292763: conti
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Matches 58; Conservative
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AKRAAGKPPATRP"
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 58958)
Sulston,J.E. and Waterston,R.
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Goyea, E. and Kozlowicz, A.
The sequence of Homo sapiens BAC clone RPII-616K2
                                                                                                                                                                                                                                                                                                                                                                                          /note-"Start codon is not identified." /codon_start*1
                                                                                                                                                                     /clone-"fj02442"
/tissue_type-"brain"
/clone_lib-"pBluescriptII SK plus"
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Genome Res. 8 (11), 1097-1108 (1998)
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/db_xref+"taxon:9606"
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                                         Location/Qualifiers
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Waterston, R. H.
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Waterston, R.H.
          Fax: +81-438-52-3914)
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Matches 57; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HKI Tear); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mall:genomicséhri.co.)p, Tel:81-438-52-3985) Manil:genomicséhri.co.)p, Tel:81-438-52-3985, Manil:genomicséhri.co.)p, Tel:81-438-52-3986) Menistry of Economy, Trade and Industry of Japan; cDNA 1011 Insert sequencing: Research Association for Biotechnology (RAb): cDNA library construction: Helix Research Institute (HKI) (Supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: HKI, and Biotechnology Center. National Insert sequencing: RAB, Evaluation: clone selection for full fusert sequencing: HKI and KAB; annotation: HKI and KAB.
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Prediction of the coding sequences of unidentified suman genes.
XVI. The complete sequences of 150 new cDNA ciones from brain which code for large proteins in vitro
DNA Res. 7 (1), 65-73 (2000)
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Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Kesesich Institute,
Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Kesesich Institute,
Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Kisarazu, Chiba
292-0812, Japan E-mail.cdnaintokazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel::61-438-52-1913,
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Mammalia: Eutheria; Primates: Catarrhini; Rominidae: Homo.
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clone:fj02442.
Shiohata.N., Matsumoto,K., Hirano,M., Sano,S., Norura,R., Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama, H., Yoshikawa,Y., Matsumura,Y., Motiya,S., Chiba,E., Momiyama,H., Yongawa,S., Raeriyama,S., Satoh,I., Matsunawa,H., Takahashi,E., Faradoxa,R., Kuga,N., Kuroda,A., Satoh,I., Kamaria,K., Takahashi,S., Sato,H., Ota,T., Watanabe,M., Sugiyama,T., Irice,S., Olsuki,T., Sato,H., Watanathio,Y., Satok,M., Nishikawa,T., Kimuri,K., Yamashita,H., Mutsuma,M., Murakawa,T., Kimuri,K., Yamashita,H., Wagatsuma,M., Murakawa,T., Kimuri,T., Takahashi-Fulii,A., Saliyama,A., Kawakami,B., Suzuki,Y., Susano,S., Nagahari,K., Masuho,Y., Nagahari,R., and Isogai,T.
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100.0%; Pred. No. 4.5e-20;
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/clone_lib="BRAWH2"
/note="cloning vector: pMEl8SFL3"
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/db_xref="taxon:9506"
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|2812, .12847
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20580. .20619
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1371. .9406
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9446. .9521
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2882. .12905
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[2956, 13033
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5604. .16018
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3542. .13571
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5456. .6558
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6218. .6301
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13574. .14658
                         /rpt_family-"(CA)n"
3527. .3778
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9052. .9381
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6665. .6818
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17729. .17946
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9864, ,19A92
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6306. .6401
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20592. .20897
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9170. .9216
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20322, 20521
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[2394. 13529
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23205. 23501
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|1924. .11974
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23502. .23593
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4706. .15418
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5025. .15140
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18286. .19823
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7818. .17867
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Submitted (09-JAN-2002) Department of Geneties, Eastimation
Submitted (09-JAN-2002) Department of Geneties, Eastimation
University, 4444 Forest Park Avenue, St. Lones, Hissouri 631/6, 18A
on Sep 30, 2001 this sequence version replaced q :15738789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The RPCI-11 human BAC library was made from the chood of one male denor, as described by osocawa K... wown, P.V., Zharo, B., Frenden, E., Tateno, M., Catanese, J.J. and de Jong, P.J., (1998), An improved approach for construction of bacterial artificial curomoscie libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resqen.com) - r Picter de Jong and coworkers at the Roswell Park Cancer Institure (http://bacpac.med.buffalo.edu)
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Actual start of this clone is at base position 1:4274 of RF5-997N5, actual end is at base position 4:275 of RP11-54E21.

Location/Qualifiers
1. 58958
                       Submitted (30-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park markway, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                             Center: Washington University Genome Sequencina Center
Center code: WOSS
Web site: http://genome.wustl.edu/qsc
Contact: sapiensfwatson.wustl.edu
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/db_xref-"taxon:9606"
/chromosome="7"
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/clone_lib="RPCI-il"
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/rpt_family~"L2"
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                                                                   MO 63108, USA
5 (bases 1 to 58958)
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AC069314 104906 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone CTD-2300122 from 2, complete sequence.
AC069314
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 3, 2002 this sequence version replaced g1:16924147.
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1 (bases 1 to 10490).
Sulston, J.E. and Materston, R.
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                                                             Length 91937;
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Desal,A., Mcyer,R. and Boyer,E.
The sequence of Homo sapiens BAC clone CTD-2300122
Unpublished (2001)
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Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                           DB 9;
6e-20;
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Genome Res. 8 (11), 1097-1108 (1998)
                                                             2.0%; Score 57; DB 100.0%; Pred. No. 6e-ative 0; Mismatches
26999 a 20814 c 19555 g 24539
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Waterston, R.H.
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Waterston, R.
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                                                               Query Match
Best Local Similarity
Matches 57, Conserv.
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Finishing Completed at Stanford Human Genome Center and Los Alamos
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On Aug 24, 2002 this sequence version replaced di:8569823.
Draft Sequence Produced by DOE Joint Gename Institute
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Mammalia, Eutheria, Primates, Calarrhini, Burnadae, Romo.
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DOE Joint Genome Institute, Stanford Human Jenome Setter and Los Alamos National Laboratory.
Direct Submission
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Homo sapiens chromosome 16 clone RP1i-141Ni4, complete sequence.
AC131566 AC017012
AC131566.1 GI:22474847
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FOE Joint Genome Institute, Stanford Human Semonne Center and
Alamos National Laboratories.
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Quality: Phrap Quality >-40 99.6% of Swquence:
Estimated Total Number of Errors is 9.2.
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Pred. No. 5.8e-20;
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Matches 57; Conservative 0; Mismatches
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/db_xref="taxon:9606"
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/clone="RP11-141N14"
                                        /rpt_family~"(TTA)n"
25228. .25597
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                                                                                                                                                                                                                                                         /rpt_family="(TG)n"
26858. .27440
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29832. .30494
                                                                                 /rpt_family="MaLR"
25916. .26051
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26089. .26270
/rpt_family="MIR"
25164, .25201
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29491. .29831
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27948. .28316
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30510. .31152
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26742. .26765
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29272. .29490
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28837. .28875
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5

Louis

/rpt\_family\*"AT\_rich" 9608. .9737 /rpt\_tamily\*"Mariner" 10067. .10098

/rpt\_family="(T)n" 10685, .11002

/rpt\_family-"Alu" 11040. .11347 rpt, family-"Alu"

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The library contains cloned BNA from human sper. See: Shizuya et al., Proc. Natl. Acad. Sei. BS 858794-7 (1992): U.J. Kim et al., Geognics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resqen.com).
MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for Genetics, Washington University, St. Louis
MOPERSON, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/4sc
                                                                                                                                                                                                                                                                   NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-498MI1, 2000 bp overlap:
the clone sequenced to the right is AF225899, 2000 bp overlap.
Actual start of this clone is at base position 142439 of
RP11-498MI1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="Alu"
1880. 1902
/rpt_family="(cAAA)n"
2027. 2621
/note="Similar to Mus musculus ES: BEAR2ARE
(ND:q16496123)*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="CT-rich"
8380. .8415
/note="Similar to Homo Saprens EST 5F972827
8708. .8743
                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 104906
/organism="Homo sapiens"
/db_xref="taxon:9606"
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8874. .9191
/rpt_family="Alu"
9177. .9221
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2751. 3006
7rpT_family-"1.1"
850. 3661
/rptC_family-"1.1"
4670. 4696
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9319. .9607
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9217. .9318
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="2"
/clone="CTD-2300122"
/clone_lib="CTD"
607. .892
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997. 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="MalR"
1599, .1900
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5431. .6627
                                                                                                                                                                                                                                            Selection: chloramphenicol
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/rpt_family-"MIR"
1376. .1424
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7465, 7710
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9579. .9617
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8316 .8420
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893. .937
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/rpt\_tamily="(CA)n" 14966. 15383

/rpt\_family="L,1" 15535. .15577

rpt\_family="(CAAA)n" 2184. .12495

/rpt\_tamil 12467. .124

/rpt\_family="(TAAA)n" |1353, |11275 rpt\_tamily="AT\_rich" (2077) ... 19nak

1318.

/rpt\_family="AT\_rich" 16302. .16354 /rpt\_family="(TTCA)n" 16326. .16402

/rpt\_family="ERV1" 18319. . 18621

'rpt\_family-"Alu" 9730. .19766

16326. 16402 /rpt\_family="L2" 17576. 18132

rpt\_family-"AT\_rich" 5549. .15680

15680

/rpt\_family="Alu" 16050, 16086

2.0%; Score 52; DB 9; Length 164996; guille, Pred. No. 6e-20; vol. 0; Missatches 0; Indels 0 /rpt\_family-"Af\_rich" 22370. .22646 /rpt\_family="AT\_rich" 24638. .24749 rpt\_family="T-rich" 9735. .20044 /rpt\_family="(CA)u" 25189. 25484 / AT\_ri. 22646 /rpt.family-"Alu" 22804, 23004 7 pt\_tamily="MIR" 24815, 2400" 77pt\_family="MIR" 24991, 2507 /rpt\_family-"ERV1" 25007. .25071 /rpt\_tamily-"Alu" 21134, .21354 'tpt\_tamily\*"MIR" 22103. .22189 /rpt\_tamily="Alu" 22354. .22386 /rpt\_family="Alu" 25694, .25983 rpt\_family="MIR" <156. .23176 rpt\_tamily="1.2" Guery Match Sest Local Similarity 160.0%; Pr Matches 52, Conscribative 0; 20044 25071 repeat\_region repeat\_region repeat, region repeat\_region repeat, region repeat\_region repeat\_region repeat\_region repeat\_region repeat, region repeat\_region repeat\_region repeat\_region

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Submitted (22-MAR-2006) Production Sequencing Farility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Mammalia: Eutheria: Primates: Calarrhini; Homioldae: Homo.
1 (bases 1 to 11614)
DVE Joint Genome Institute.
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Homo sapiens chromosome 16 clone CID-2169K.9, cosquence.
ACO26423
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Homo sapiens BAC clone CTA-437235 from Eq21, cosplete sequence
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Submitted (04-JAN-2002) Production Sequencing Pacility, UDE., Submitted (04-JAN-2002) Production Sequencing Pacility, UDE., Genome Institute, 2800 Mitchell Dirace, Walfill, Creek, CA 9459 on Jan 4, 2002 this sequence version replaced dilt484459. Sequence Quality Assessment:
This senty has been annotated Will: Sequence quality as computed by the Phrap assembly program.
All manually edited bases have been reduced to have less than outlity levels above 40 are expected to have less than 1 error in 10,000 bp.
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This entry has been annotated with sequence quality estimates computed by the Phrap assembly prouter.
All manually edited bases have been reduced to positive Quality levels above 40 are expected to have also then I error in 10,000 bp.
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100.0%; Pred. No. 6.1e-20;
tive 0; Mismatches 0;
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/db_xref="taxon:9606"
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DGE Joint Genome Institute.
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between originaring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems,
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 11650)
Ozersky,P., Holmes,A. and Broy,M.
The Sequence of Homo sapiens BAC clone CTA-437L15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The clone sequenced to the left is CTA-237Gl. The actual start of this clone is at base position 1 of CTA-437L15; actual end is at 116650 of CTA-437L15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wastington
Missouri 53168,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missouri 63108,
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This chromosome 8 clone was provided by Dr. Patrick Concannon
(patconwunnciorg) at the Virginia Mason Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as compressions and repeats: all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (21-EEC-1999) Department of Genetics, Washington
                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                               Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Genetics,
Park Avenue, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University, 4444 Forest Park Avenue, St. Louls,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone contains STS HS275YF1 (NID:91051703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web size: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: H_RG437L15
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/db_xrel -"taxon:9606"
/chromosame-"8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-JUN 1998)
University, 4444 Forest
4 (bases 1 to 116650)
Waterston, R.
                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (15-JAN-1998)
                                                                                                                                                                                                                                                                                                                                                                      University, 4444 Forest.
3 (bases 1 to 116550)
                                                                                                                                                                                                                                    (bases 1 to 116650)
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HS329A5 linear PRI 01-FEB-2000 bnA linear PRI 01-FEB-2000 bnA sequence from clone RP3-329A5 on chromosome 6p21.1-21.33 Contains a pseudogene similar to ribosomal protein i.5sa, ZNF76 (zinc finger protein 76 (expressed in testis)), part of the gene for KIAA06460 protein, an EST, STSS, GSSS and CpG Islands.u,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1025 CTCACTGTAACCTGTGCCTCCCGGGTTCAAGCGATTCTCCTGCTGCTCAGCCTCCTGAG 1081
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188.0%; Pred. No. 6.1e-20;
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35994. 36286
/rpt_family="Alu"
36686. 36985
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31761. .3195s
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43357, 41450
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32329. .32460
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34525, 34930
  /rpt_family~"MER1_type"
26268. 26500
/rpt_family~"MER1_type"
26611. 27000
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34999. .35256
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44088. .44386
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11956. 32225
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41954. 42006
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33155. .33281
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34433. .34514
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15388. .35477
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17488. .37673
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s8297, s8500
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29435. .29752
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31170. .31344
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30205, 30341
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37862. 38161
                                                                                                 /rpt_ramily-"Ll"
28128. 29109
                                                                                                                                                 /rpt_family."Ll"
29128. .29434
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12596. .42777
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297832
297832::1 01:6065887
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HS329A5/c
LOCUS
DEFINITION
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KEYWORDS
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70te="MudSC18"
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TWEVLSRKOPFEDVTNPLQ1MYSVSGHRPVINFESIPYTTFHEMRHSISLIFSGWAQN
PDERPSFEKCLIELEPVLENFEETTFEETTEMVIGURYSTRAGSVSSATHLFTRKKWELSLN
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MTEACHNGSLDALLSROLIMKENFILVSTRYNPTHYSKVRQLITTLIGGGEEFAKVIVQK
14 CANNOMINGLOPYPETLVYSRSPSLNILGNKSM"

18 770
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6133. .6433
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10435. .10540
/clone_lib~"CITB-HS-A"
150. .530
                                                                                                                                                                                                                                                /rpt_family="(TA)n"
3845. .4563
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16292. .16429
/rpt_family="L1"
16460. .16991
                                                                                                                                                    /rpt_family="Mal.k"
3188. .3348
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7110. .8040
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11433. .11538
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23929, .24439
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25337. .25671
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11790. 12003
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12466. 12557
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15579. .16292
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5641 6075
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22863. .23483
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24471. .24960
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24967, 25285
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26151. .26280
                     /rpt_family="L1" 498. 640
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23575, .23750
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23761. .23924
                                                                                                 /rpt_family-"L1"
673. .1096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://bacpac.med.bufalo.edu/
VECTOR: pCYPAC2
IMPORTANT: This sequence is not the entite insert of clone
IMPORTANT: This sequence is not the entite insert of clone
RP3-329As It may be shorter because we arrange for a small overlap
sections once, or longer because we arrange for a small overlap
between neighbouring submissions.
The true left end of clone RP3-329As is at 1 in this sequence. The
true left end of clone RP3-329As is at 1 in this sequence.
This sequence was generated from part of bacteria. clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
Mapping Group. Further information can be found 4:
http://www.sanger.ac.uk/RGP/Chr6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence subrission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL: SWISSPROT, Tr., TEMBLE, WP:, WORPEP, Information on the WORMPEP database can be found at
                                                                                                                                                                               Submitted (OLFBE-2000) Sanger Centre, Hinxion, Farbridgeshire, CEBO 18A, UK. E-mail enquiries: humqueryssanger.ac.ac. clonerequest(%anger.ac.ax requests: clonerequest(%anger.ac.ax concrete) 1999 this sequence version replace; q:5556482. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu), Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP3-329A5 is
from the library RPC1-3 constructed at the Roswell Park Cancer
Institute by the group of Pieter de Jong, For Larther details see
                                                   Eukaryota, Metazoa, Chordata, Graniata, Verlebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Rominidse, Homo.
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342. .981.
/note="20 copies 2 mor 91 77% conserved"
11477. .11646
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//note="match: GSS: Em:AQ416819"
18510, 18912
/note="match: GSS: Em:Ay762944*
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    117026
    /organism="Homo sapieus"
/db_xref="taxon:9605"
    /chromosome="6"

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/clone="RP3-329A5"
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Williams, S.
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9342.
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/note="40 co
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AUTHORS
TITLE
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SOURCE
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match: cDNAs: Em:X52966
match: proteins: Mp:CE04362 Sw:P02434 Sw:P18077 Sw:055142
Sw:P046465
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48209
/note-"charlie2 repeat: matches 3554. .3577 of consensus"
48236. .48515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46481. 47711
/note-"Charlie2 repeat: matches 1826. 3213 of consensus"
47781. 47913
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/note="Charlie2 repeat: matches 3577. .3760 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.351. .46459
//note-*Charlic2 repeat: matches 174. .285 of consensus*
46481. .47711
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/note-"Single clone region. Small insert library of pUC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"FLAM_C repeat: matches 27. .111 of consensus" complement(66719. .67074)
/note-"match: GSS: Em:AQ128487"
                                                                                                                                                                                                                                                                          .175 of consensus"
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    .196 of consensus?
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complement(55446, .55894)
/nore-"match: GSS: Em:AQ782507"
55895. .56146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="75K repeat: matches 5, .110 of consensus" 63578. .63629
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/gene="dJ329A5.1"
                                                                                                                                                                                                                          /note="15 copies 2 mer ga 86% conserved" 31101. .31220 /note-"MEK91A repeat: matches 52. .175 of 35578. .35884
                                                                                                                                                                                                                                                                                                                                                                                                       /note="129 copies 2 mer et 69% conserved" 41817. 41842
7. Arcte="13 copies 2 mer tt 92% conserved" 45456. 45517
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/note-"15 copies 2 mer aa 86% conserved"
60851. .60960
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64340. .64598
                                                                                                                   25974. .zouju
/note="3 copies 19 mer 87% conserved"
30570. 30726
                                                                                                                                                                     /note="3 copies 19 mer 86% conserved" 30703. ,30732
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/gene-*dJ329A5.1*
/note="MER91A repeat: matches 90.
21086. .21547
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/note-match: GSS: Em:AQ455275*
39952. .40009
                                      /note="match: GSS: Em:AQ506253"
25158. ,25441
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                                                                                      /note+*match: GSS: Em:AQ771827*
25974. .26030
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/wote-"match: GSS: E057730. 57793
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/note-"CpG island"
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Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 58 of reads
Sequencing vector: M13; M77815; 58 of reads
Sequencing vector: plasmid: L08722; 948 of reads
Chemistry: Dye-terminator ET-amersham; 28% of reads
Chemistry: Dye-terminator ET-amersham; 28% of reads
Consensus quality: 108370 bases at least Q40
Consensus quality: 112560 bases at least Q20
Consensus quality: 11458 bases at least Q20
Insert size: 125703; sum off-contigs
Insert size: 198549; 0.6% error; agarose-fp
Quality coverage: 3.40x in Q20 bases; sum-off-contigs Quality
coverage: 2.66x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
On Sep 9, 2000 this sequence version replaced gi:9864236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig of 11131 bp in length p of 100 bp contig of 3957 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2888 2987; contig of 2887 bp in length 2888 2987; agap of 100 bp 6255 6354; gap of 100 bp 100 bp 6255 6354; gap of 100 bp 100 bp 8455 8455; contig of 2101 bp in length 8556 19953; contig of 2398 bp in length
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gap of 100 hr
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gap of 100 hm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24423: contig of 2734 bp in length 23: gap of 100 bp 26757: contig of 2234 bp in length.
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contig of 4050 bp in length
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49182: contig of 2675 bp in length
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41: gap of 100 bp
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                                                                                                              Contact: humquery@sanger.ac.uk
                                                                   Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                           Center project name: bA57Bll
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10954 11053; gap of
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                                             Center: Sanger Centre
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  COMMENT
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TVPGGGKRFTEYSSLYKHHVVHTHCKPYTGSTGGKTYRQTSTIAMHKRSAHGELEATE
ESEQALY EQQQLEAASAAEESPPPKRPRIAYLSEVKFERIUT PAQVAMYTEEKGAPQV
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DGTOTOPOYTIISGAVVAEDSSVASLRHQQVALLATANGTHIAVGLEEGGTLLEFAINV
ATAAHQQGAVTLETTVSESGG"
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testis))"
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Eukaryota, Metazoa, Chordata, Graniala, Verlebrata, Esteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Gambildeshire,
CBIO ISA, UK. E-mail enquiries: humqueryesanger.ac.uk Clone
requests: Clonerequest@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"MER53 repeat: matches 122, .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1025 CTCACTCTAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGGCTTCAGCCTCGTCAG 1081
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5.le-20;
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Mclay, K.
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AUTHORS
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SOURCE
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74868 78453: contiq of 3586 bp in length. 78454 7853: gap of 100 bp 78554 84138: contig of 5585 bp in length. 84139 84238; qap of 100 bp 84239 91282 91381: qap of 100 bp 96605 96704; qap of 100 bp 96705 105604: contig of 8930 bp in length 105605 105704: qap of 100 bp 100 bp 105705 108501: contig of 2797 bp in length 105802 108601: gap of 100 bp 100 bp 108602 112313: contig of 3730 bp in length. 112332 112431: qap of 100 bp 100 bp 108603: qap of 100 bp 100 bp 108603: qap of 100 bp 100 bp 112332 112431: qap of 100 bp 100 bp
74867: gap of 100 bp
7453: contig of 3886 bp in length.
7853: gap of 100 bp
84138: contig of 5585 bp in length
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1. 2867
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Attori.M., Ishii.K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,I., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
AL Published only in Database (2001)
SS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T. Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
AL Su
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Homo sapiens genomic DNA, chromosome 11q, clone:RP11-626412,
Complete sequence.
AP003555
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Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Query Match 2.0%; Score 57: D8 9: Lenith 121600; Bost Local Similarity 100.0%; Pred, No. 6.16-20; Matches 57: Conservative 0; Mismatches 0; Lidels 6; daps

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AT. I GINMENTS

Human ABC1 transcription regulatory DNA #1. AAD37265 standard; DNA; 3231 BP. 21-AUG 2002 (first entry) AAD37265; RESULT : AAD37265

Homano ATP-Economy cassette 1: ABC1 gene regulation, atheroscierosis; cholestero, metabolism; hypercholesterolaemia; antisense therapy; ds.

Homo sapiens.

02 MAY-2091; 2001WO-EP05488 02-MAY-2000; 20000S-201280P. W0200183746-A2 08 - NOV - 2001.

Denefie P; ROSier-Montus M. Prades C. Lemoine C. Naudin L. Den Brower B. Doverger N. Remaley A. Santamarina-Fojo S; (AVEL ) AVENTIS PHARMA SA. WPI: 2002-154464/20. 

Isolated nucleus acid useful for modifying the ATP-binding cassette I (ABCI) and serecting for candidate modulatory compounds or substances

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The invention relates a nucleur acid which is capable of requisiting the transcription of human ATP binding cassette [ (ARCI) gene, which, is a casual gene for pathologies linked to a dystimetromina or chalasteries of the invention are used to serven candidate molecules or sensioned of the invention are used to serven candidate molecules or sensioners what are capable of modulating the transcriptions of the APC gene, the APC gene research in service used in antisense therapy. Compositions comprises a sension the invention are used to treat hypercholesterolaumia and attacks where its The present sequence is human ABC1 transcription regulation law Page 130-131; 152pp; English. Claim 1; 

Segrence (231 BP) 809 A: 773 C; 876 G; 733 L; C other,

=: -G(15) 560 1 121 CLICAGOCCAGAGGATCGCTTGAGCTCCAGAGTTTGASACVASCOLOGALAACALGGAAA 480 FIDELITIETTITETTITETTITETTITETTITETTETTETTITETTITETTITETTITETTITETTITETTI CINANCOATGATTGGATCACTGCACTCCAUCTLOGIAGACAGGAAGACATGTGTGA 660 GOCCAGATOGCACTGCACTCCAGCTGGCACAAAAAGGTGAAAGTGCATCTGAATT 1,20 Ş ACCITG FCTCTACAAAAAAAATACAAAATTAJAJGGSFCFCGCGCGATGFACTGTGSF 54F ĵ. AND CONTROLLED OF AN ARCOCOT FIGAROAN ANAMATATAN AND CONTROLLED AN LITAATAACACTCTCTCCTTTTATAACATCTTTCTGPPAAGGGGCTCAAAGGTTTGAAGA (61 AASATGAAGAAACAGGCCGGGCACAATGGCTAATGCCTGTAATGTCT AGGAAGTT GCGASG THEFT HELLET HE HELLET HELLET HELLET HELLET HELLET HELLET HELLET HELLET HELLET AGAFGGAGGGTCAGGGAGA ICTAATT ACTC 10 PAAAA 10 ATAGG TAGGAAGA 1 AAGAA 10 1 CCCAGCTACT FGGGAGGCTAAGGTGGGAGGATCCT (GARRYCAGGGAGTCAAGTCLAYA <u>:`</u> Leingt L Indels 108 24; 100.0%; Score <231; 100.0%; Pred. No. 0; ive 0; Mismatches Best Local Similarity 100. Matches 3231, Conservative areny March <u>=</u> 8 100 171 <u>2</u> 5 <u>3</u>. ź 3 Ξ 3 Ξ 3 Ξ ò ŝ 3 Ē 3 ŝ 3 ŝ 9 ò â ŝ £ 3 ŝ ŝ 3

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                                                                                                                                                                                                                                                                                                                                                                               High density impoproteis cholesterol, HDL-C, cardiovascular: ABCl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention relates to a method for treating a patient diagnosed as having a lower than acromal high density impoprotein cholestern (MDL-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXR- or RXR-mediated transcriptional activity or ARC] expression or activity. The LXR gene product may be used in an assay to identify
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lower than normal HDE, cholesterol level, a higher than normal
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The present sequence represents the 5' tlanking region of the human adenosine tripmosphate (AIP) binding cassette protein (ABC) i gene. ABC1 resides in cell membranes and utilises ATP Mydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a protein a variety of substrates across the plasma membrane. ABC1 is a protein cholesterol in the apolipoprotein-mediated mobilisation of in racellular cholesterol in the apolipoprotein-mediated mobilisation of in racellular cholesterol in the apolipoprotein-mediated mobilisation of in racellular cholesterol metaholism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are also idealy pharmacoutical agents for the instance of proteins are after disease and other disorders associated with hypercholesterolesis and atherosclerosis. The genes acrossited with hypercholesterol transport. The genes and proteins are also useful for are also useful for are also useful disorated with hypercholesterolemia.
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The present sequence represents the 5' flanking region of the hussan adenosine 'tiphosphate (AIP) binding cassette protein (ABC) I gene. ABCI resides in Celi Ecomptanes and utilises ATP hydrolysis to 'transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolip-profein-inediated mobilisation of intracellular cholesterol states. ABCI is detective in Tangler disease, a genetic disorder characterised by abnormal BDL-cholesterol metabolism. The ABCI genes and proteins are used, for disconding pharmacrafized agents for the treathern of healt disease, and other disorders associated with hyperrholesterological
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The invention relates to an isolated human large ATP-binding cassette transporter i (AbC) promoter capable of directing transcription of therefore capable of directing transcription of promoter is used; but expressing toreign DNA in a host cell, by introductualists the most cell a gene transfer vector complished the promoter operaty tinked to a foreign DNA encoding a desired polypeptide of NA, where the tolerand DNA is expressed. The gene transfer can be introduced into the lost cell by additional infection, theseme-mediated transfer. I goal application to the cell or microinjectuse. The gene
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transfer vertor encodes and expresses a reporter molecule. The method

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further involves introducing into the cell a gene transfer vector comprising a nucleic acid segment encoding a transactivator protein rapidite of uprogulating the ABCI promoter, or contacting the real with the transactivator protein, or an agonist, of the transactivator protein. Medulators of human ABCI gene expression are useful for freeding atheroscletosis. The present sequence represents the MaSCI promoter.
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27 AUG 1999;
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The present invention describes primer sets for synthesising 5602 tuli-length cDNAs detrined in the specification. Where a primer set comprises: (a) an object? Primer and an objeoucleocide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 cucleotide comprises at least. Is nucleotides; or (b) 4 combination of an objeoucleotide comprises a sequence complementary to the comprise of a sequence complementary to the comprise of a polynucleotide which comprises a 5'-end sequence and an objeoucleotide comprises a sequence complementary to the comprises an objeoucleotide comprises and sequence complementary to a polynucleotide which comprises all-east 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in quene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the private of the full-length cDNAs. The primers are also useful for the connection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for the cDNA easily without any specialised methods. AAH13629 to AAH13629 to AAH13632 represent thuman amino acid sequences; and AAH13632 to AAH13632 represent configences and an anioa acid sequences; and AAH13632 to AAH13632.
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ilarity 100.0%; Pred. No. 1.5e-61;
Conservative 0; Mismatches 0; Indels 0;
                                                      Saito K, Ya
Otsuki T;
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                                                              Hayashi K, S
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Sugiyama T. Wakamatsu A,
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Best Local Similarity
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  2000US-0251869.
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the present invention provides the protein and coding sequences of 973 human testicular autiques, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, respiratory, neurological and gastrointestinal disorders, intections, and particularly cancer, especially testicular cancers. The present sequence is a DNA checking a
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51.2%; Pred, No. 3.7e-60;
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The invection relates to novel genes (ABA11004-ABA21534, and proteins (ABB14678-ABB18001) useful for preventing, treating or amelicating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis. Treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, tone, bone marrow. breast, qustrointestinal tract. liver, lung, or urbleantial; (b) immune disolders and other cancers of the adrenal gland, tone, bone marrow. Breast, autoimmune thyroiditis, diabetes mellings, Croim's disease, multiple sclerosis, rheumatoid arthritis and nicerative collisis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and englieby; and (f) miectious diseases such as viral, bacterial, trugai 280 / GCTAGCCAATGAAAATGTGATTAATGGACTTATCAGGCTAAGACT---GCCTTAAGCTG 2747 Nucleic acids encoding 324 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system (71 791 2863 AMGTCAAGGAAGGTTGAGGATGTITTACCAATTATTTTAAAGTCTAAAGTGAGAAAGGG 2804 435 TOSCETORACIO CAGASTITICAGACCAGCCAGGATAACATGGCAAAACCCTGTCTCTACA 494 375 GGCCGGCCACAATGGCTAATGCTCTAATCCAGCACTTTGGGAGGCTGAGGCAGAGA 434 printed specification, but was obtained in electronic formal directly from WIPO at 11p.wipo.int/pub/published\_pct\_sequences. Pred. No. 2.8e-60; 0: Mismatches 299; Indeis i7; Gaps AGBITTAAGG LOJOAGGA FOOTT FGAGCCCAGGGAGTCAAGTCTAGAC FGAGCCATGATTG GGTAGAAAGACTTTACCTAAATTGCTCATGTGGTTGTCAAGTTTGACCCCAAAAACCC DB 22; Length 5076; Disclosure; SEQ ID NO 9030; 1701pp + Sequence Listing; Endlish Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic tormal Sequence 5076 BP; 1435 A; 1052 C; 1191 G; 1398 T; 0 other; 10.28; Score 330.6; 65.0%; Pred. No. 2.8 Ruben SM (HUMA-) HUMAN GENOME SCI INC. 08-DEC-2000; 2000US-0251990; 11-DEC-2000; 2000US-0254097; 05-JAN-2001; 2001US-0259678; and parasitic infections. Best Local Similarity 65.09 Matches 587; Conservative cancers and metastases Barash SC, WPI: 2001-541565/60. Rosen CA, Query Match 555 g Š 2 ŝ ŝ 5 3 ŝ 3 5 3 3 ŝ င် Ê

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20000S 02245.8 20000S-0224513 20000S-0225213 20000S-0225264 20000S-0225266 20000S-022526 20000S-022526 20000S-022526 20000S-0225268

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Nucleic acids encoding 3224 haman nervous system antiger polypoptides, useful for preventing, diagnosina and/or freating nervous system cancers and metastases.

Disclosure, SEO ID NO 9032, 1701pp · Sequence tusting. English.

Isolated from a range of fundant issues discissed in the specification. The anclete acids, proteins, antibodies and (antibacensis are used). In the diagnosis, treatment and prevention etc. (a) cancers e.g. breast and ovarian cancer and other cancers of the adread alrad, tank, then the marrow, breast, gastrointestinal fract, liver, ind. or moranital, (b) immure disorders e.g. Addison's discuss, allerates medicities, rethermalisments anatomical. The invention relates to movel genes (ABALL) 4 ABALLS4, and proteins (ABAL4678-ABB18001) useful for preventing, treating or americal medical conditions e.g. by protein or gene therapy. The genes are disease, muitiple sclerosis, rheumate, Jarthritis and unequalize

2852 AAGICAAGGAAGCTICAGGAICTTITACCAATTATTITAAAGTCTAAAGIGACAACCIA 2803 1032 TAAGGTGTGGCTTCCCGGGGTTCAAGCGATTGTCCTGCTCAGCCTCCTGA------GAT 1083 1204 CCAAAG-TSS FSS FSS FSAGATGA AGA TGA GCAA CTGC GC CCAACCTA AGA TCC TTTCT 1262 PER HELLE TELLET FELLET colitis; (c) cardiovascular disorders such as myocardiar ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) intectious diseases such as viral, bacterial, fungal in S 191 852 ANTITATIBAMAAN DIDATENTITGATIGAGGAAGGGGGTCCGCTCTGGGCTIG 911 971 directly 375 GOLDGUSCANTANIGGCTATANICCARGAGEACTITGGGAGGCTGAGGCAGAGGA 434 435 Teserrandicendantireagacendentegarearacetegeaaacetetera 494 .7; Gaps 3102 CTAAAAATACAAAAA1TAGGCAGGCATGGTGGCAGGGGGGCTGTAATGCCAGGTACTGAGG 2922 AGAGAGAAAAAGAGICTTGATAAGGAACTTGGGATAACTAAATAATTTGGAAGATAAA 912 GOCTIIAGAAAGGICATGIGIGGGGIITCTGAGATCCAICCTTICTTTTTTIITTCII 495 AAAAAAATACAAAAATTAGATGGGTGTGGGCATGCACCTGTGGTCCCAGCTACTTGGG 555 AGGCTAAGGGGGGGGGGGGTGGGTTGAGGCCCAGGGAGTCAAGTCTACACTGAGGCCATGATTG 792 GGCAGAAAGACTTFACGIAAATTGCTCATGTGGTTGTCAAGTTTGACCCCAAAAACCC 615 GATCACIGGACTCCAGCCIG---GCTAGACAGAGACCCTGTCTCAAAAAAAAAAA 10.1%; Score 325.8; DB 22; Length 5075; 64.7%; Pred. No. 2.9e-59; Note: The sequence data for this patent did not form part of printed specification, but was obtained in electronic format Sequence 5075 BP: 1437 A: 1654 C: 1187 G: 1397 T: 0 other; from WIPO at ftp.wipo.int/pub/published\_pct\_sequences. Mismatches 302; ; 0 and parasitic infections. Conservative Local Similarity Matches 584; Query Match 3 33 â 43 S Ct ô 35 3 â οž ä 3 Ξ 3 š â 3 3 ä S. ŝ 5 3 ŝ 88888888**8**8 ŝ ð ŝ 3 Š

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The invention relates to detecting (MI) frame cast (MI) attributed (GMA), by setering the level of ceases as there as (MI) attributed (GMA), by setering the level of ceases as there as (MI) attributed (MI) at a cast (MI) at the expression level to an expression of MI) at the cease (MI) attributed (MII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       example, they may be used to treat disorders associated with dorneased expression by rectifying mutations or deletions in a patient significant brainful affect the activity of (1) by expressing interview protects on to supplement the patients on production of (1). Additionally, (1) polynocleotides may be used to produce the secreter (1), by inserting the rucleur actus into a host coil and cultiminates the protect. (1) proteins and polynocleotides may be used to precent, proteins and polynocleotides may be used to precent, diagnose and treat immune/harmatopolicities elasted a seaso, especially cancer metastases of harmatopolicities.
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                                                                  18025 GAAAAGAAAAAAATAATCAAACAGGAACTTAAGACATTCTAAGCCAGTACATATCTCAA 18084
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AATGAAAGAGAAAGAAAGAGGGAGAGAGGAGGAGATGAGGGGAGG-----AGGGGAGG 724
                                                                                                                                                                                              18085 TTAGCTTAGTGAGCTTGGGCCAAAACTTTAGAGCCAAATTCCTCAACTATATAAGAAGAG
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sedical conditions e.g. by protein or gene therapy. The generalical soluted from a range of human tissues discipaced in the specification, antibodies and (ant)agonists are issuid in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adread sland, bone, bone marrow, breast, dastrointestinal tract, liver, hum, or momental:
(b) immune disorders e.g. Addison's disease, alterates metits. Croin's disease, multiple sclerosis, rhemmator after a utoimmune thyroidiis, diabetes metits. Croin's disease, multiple sclerosis, rhemmatoria after a section of a cardiovascular disorders seed a section (d) wound healthap (e) neurological disvasce e.g. evertes a mycratical discipantials) (s) equipassy and (1) infectious diseases such as viral, british, immal
                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not four part of the principal principal specification, but was obtained in electronic force directly from Wife at ttp.wipo.int/pub/published_pet_sequences.
                                                                                                                                                                                                                                                                                                                                                                           and parasitic intections.
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Sequence 23934 BP; 7785 A; 4761 C: 4365 C; 7923 T; 7 offer:

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                                                                                                                                              SGF5 : 5.
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20630 TCAAGGGAFFCFVAIGGCFCAGGCFCCCAAGTAGGGGATTACAGGGGGATGCCACGAT 20571
                                                  1103 APCTGGCTAAT11TTGTAITPTAGTAAAGACTGGGTTTCATCATGTTGGCCAGGTTGGT 1162
                                                                        20570 GCC1GGCTAAITTTTGTATTTTAGTAGAGACAGGGTTTTAGCATGTTGGCCAGGCIGAT
                                                                                                                                                   1163 TTCGAACTCCTGACCTGAGGTGACCTCCCACCTTGGCCTCCCAAAGTGCTGGGATTACA
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9, 2003, 13:07:37 Search completed: May Sobside time: 1122.17 Sees

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AW748318 RC6-BTO25
AU135588 AU135588
AW815516 QVO-57023
AQ265389 CITB1-E1-
AQ418551 RPC1-11-2
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3231
l acagggcatggtggcaggtg......gccccacatccccaccatt 3231
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen 14d.
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Listing first 45 summaries
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                                                   OM nucleic - nucleic search, using sw model
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Dias Noto,E., Garcia Correa,R., Vertevski-Amerida,S., Briones,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Boldin,S., Gosta,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Haid,S.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Matsukuma,A., Laid,S.S., Simpson,D.H., M.J., Soares,F., Brentani,R.R., Peris,L.F., de Souza,S.J. and
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RC6-BF0252-271099-012-C10 BF0252 Homo Sapirus CiNA, mKNA Sequence.
AM748338
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This sequence was derived from the FAPESP/LECK Heman Cancer Genome
Project. This entry can be seen in the following UK.
(http://www.ludwig.org.br/scripts/gethtml2.pl2t1+895at2-RCF-530252-
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 undar. @15097010, Sap PatlorSP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2600)
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100.0%; Pred. No. 4.3e-28;
               1. .763
/organia-"Homo sapiens"
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/clone="MAMHA1000851"
/clone_lib="MAMHA1"
/tissue_type="mammary gland"
/note="Vector: pME188FL3"
7 a 205 c 260 g 158 t
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Matches 336; Conservative
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1. 289
/Ordanism-"Homo sapiens"
/Ordanism-"taxon:9606"
/Clone_lib-"B10252"
/dev_stage="Adult"
/note="Organ: breast: Vector: puo18; Site_1: Smal: Site_2:
                                                                                                                                                                                                                                          Small, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 716 - Ludwig Institute for Cancer Research) profiles into the DUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 736)
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HRI human cENA project; 5'-6 3'-end one pass sequencing: Helix
Research Institute; cUNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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Tel: 81-438-52-3975
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271099-012-c10&t3-1999-10-27&t4-1)
              Seq primer: puc 18 forward
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Contact: Takao Isogai
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/clone_lib="ST0236"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Enteleostomi,

Mammalia, Eutherla: Primates, Catarrhini; Hominidue; Homo.

1 (bases I to 457)

Dias Neto,E., Garcia Correa,R., Verjovski-Aumeidu,S., Briches,M.R.,

Nagai,M.A., da Silva,W. Jr., Zado,M.A., Burlin,S., Gosta,F.F.,

Coldman,G.H., Carvalho,A.F., Matsukuma,A., Buin,G.S., Simpson,D.H.,

Hrunstein,A., Goollveina,P.S., Bucher,P., Jongenhel,G.V., O'Hare,

M.J., Soares,F., Brentani,R.K., Reis,L.F., de Suza,S.J., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LECK Human Cuncer Genome
Project. This entry can be seen in the following UE.
(http://www.ludmig.org.br/scripts/gethtml2.Fi2tl-sf2_UV0-SF0236-171_
299-075-bl26t3-1999-12-176t4-1)
Seq primer: pur IB forward.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-518, Sao Paule-SP,
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                                               /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="ptace1002437"
/clone=lib="ptace1"
/clone=lib="ptace1"
/clone=lib="ptace1"
/note="veryee"ptace1"
/note="yeque"ptace1"
/note="yeque"ptace1"
                                                                                                                                                                                                                                     0; Mismatches
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/db_xref-"taxon:9606"
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                     Location/Qualifiers
 Research Institute
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                                                                                                                                                                                                                                       223; Conservative
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                   FEATURES
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Anote—"Organ stomach; Vector: pucl8; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
Site_2: Smal; A mini-library was made by cloning products
whereof from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
iow stridenty conditions.

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GITBL:E1 2569010.IF GITBL:E1 Homo sapiens genomic clone 2509010,
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Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-2;
Class: BAC ends.
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Enkaryotus, Mutazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 577)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                     955 TTCTTTTTATTTTTCTTGACAGGAGTCTTGCTCTGTCACTCAGGCTGGAGTGCAGTGGC 1014
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Clones are available from Research Genetics (info@resgen.com).
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1015 ATGATCTCGACTCACTGTAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCTTCAGCC 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1075 TCCTGA-----GATAACAGGGGCGGGGACCACATCTGGCTAATTTTTGTATTTTTAG 1127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  217 1GCCACCICAAAACTCCTGGGATACAGGCGTGACCACTGTGCCGGCTCT 358
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Other_GSSs: CITHI-E1-2509010.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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BQ775487 62.01.81 NCL_CGAP_FH0 Homo sapiens CDNA clone UI-H-FH0-bcj-1-24-0-UI-31 NCL_CGAP_FH0 Homo sapiens CDNA clone UI-H-FH0-bcj-1-24-0-UI-3', mRNA sequence.
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: BcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
86 c 165 g 85 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                     353 CCATTTTAAAGATGAAGAACAGGCCGGGCACAATGGCTAATGCCTGTAATCCCAGCACT 412
                                                                                                                                                                                                                                                                                                                                                                                                                                        413 TIGGGAGGCIGAGGCCAGAGGATCGCTIGAGCTCCAGAGTTIGAGACCAGCCTGGATAAC 472
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Pred. No. 3.3e-15;
); Mismatches 125;
                                                                                                 /organism="Homo_sapiens
/db_xret="GDB:7577811"
/db_xref="taxon:9606"
                                                                                                                                                        /clone="RPC1-11-203K4"
/clone_lib~"RPC1-11"
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Email: cqapbs r@mail.nih.gov
                                                           Location/Qualifiers
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BQ775487.1 GI:21983963
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Matches 306; Conservative
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TITLE
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RPCI-11-203K4.TJ RPCI-11 Homo sapirens exponente de me FEET il-Zeekk4,
DNA sequence.
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Clones are derived from the human BAC library RFCT ... FS: BAC
library availability, please contact Fieter de Johns
(Pieter dejoing.med.bulfalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.bulfalo.edu/orderiva) or tros.
Research Genet cs (infodresyen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enkaryota: Metazoa; Chordata; Craniata; Verminiana Euteleostomi;
                                                                                               /clone_lib-*CITB1.El*
/sex-*male*
/cell_type-*sperm*
/note-*Vector: pBelobACil; Site_l: &coMl; Site_2: EcoMl;
/note-*Numan BAC Library 2*
127 c 137 g 146 t
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1 (bases 1 to 544)
Thao.S., Adams,M.D., Nierman,W., Malek,J., de Jecte, and Venter
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Pred. No. 2.5e-15;
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Costact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
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9212 Medical Center Dr., Rockville,
1el: 301-838-0200
Fax: 301-838-0208
                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
      Location/Qualifiers
                                                                              /clone-"2509010"
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dbo=*UVI=FH0-bo].124.0-UI*
/clone=*UVI=FH0-bo].124.0-UI*
/clone=*UVI=FH0-bo].124.0-UI*
/tissue_type=*Human Choudrosarcona (e): Line*
/de_staqe=*Adult*
/lab_host=*DHJ0B (Life Technologies)*
/note=*Organ: Bone: Vector: pT7T3-Pac (Pharracia) with a modified polylinker; Site_1: EcoR : Site_2: Not ::
//db_host=*BHJ0B (Life Technologies)*
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//db_host=*Muman Grade | Chondrosarcomia Cell Line The library was Constructed according to Sonalao, Lenson and Soares, Genome Research, 6:794-806. Line The library was Constructed according to Sonalao, Lenson and Soares, Genome Research, 6:794-806. Land closed Containing a Not I site, Double stranded CDMA was ligated to an EcoR i adaptor; digested with an ollude directionally into pT7T3-Pac vector. The cliqonucleotide used to prime the synthesis of first strand count could directionally the synthesis of first strand count could be defined by In Janes Mattin from University of Iowa
Tissue Procurement: James Martin Contest Eliversity of Towa Cond Library preparation: Dr. M. Hento Scatus, Eliversity of Towa Cond Library Arrayed by: Dr. M. Hento Soares, University of Towa UNA Sequencing by: Dr. M. Bento Scares, University of Towa Clone Distribution: Clone distribution can be obtained
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AGENCOURT_6439541 NIH_MGC_71 Homo Sapiens cDNA clane :MAGE:55526297
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Chondrosarcoma
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The following repetitive elements were found in this clnA
sequence: 17-36, >ALU (matched compliment)
Seq primer: MIS FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1186 GCIGCCCACCTTGGCCTCCCAAAGIGCTGGGATTACAGGCATGAGTAATGCGAAAGAG
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/lab_hosta*DH108 (phage-resistant)*
/note**Organ: uterus; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally, Primer: Oligo dT
Eukaryota: Metazoa, Chordata; Craniata; Vertebrata, Euteleustomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 990)
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                                                                         NIH'MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencies by: Agencourt Blosclence Corporation
Cone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12184 row: b column: 10
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80.7%; Pred. No. 3.5e-15;
ive 0: Mismatches 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Homo sapiens"
/ub_xret-"taxon:9606"
/elone-"IMAGE:5520297"
                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cyapbs.rémail.nlh.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib-"NIH_MGC_71"
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BM991096.1 GI:19710485
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                                                                                                                       Venter, J.C.
Use of BAC End Sequences from Callech Libraries for Sequence-Roady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: hbe@tigr.org
Clones are available from Research Genetics (1813 Presqen.com). BAC
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http://www.tigr.org/tdb/humqen/bac_end_search/bar_end_search.html.
Seq primer: M19.21
Class: BAC ends.
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calred Human bBC Library D"
t 162 c 180 g 149 t
Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 893 TOCACTCICCTGGGCCTTGGGCTTTAGAAAGCICATCTGGCCTTTCTGAGAIGCAFGC 952
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                                                                                           Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shiruya, E.,
                       Mammalia: Butheria: Primates: Catarrhini: Hominidae:
1 (bases 1 to 719)
                                                                                                                                                                                                               Unpulished (1997)
Unpulished (1997)
Other_GSSS: CITBI-E1-2589B9.TK
Contact: Shaying Zhao, William Nierman, Mark Adans
Department of Eukaryotic Genomics
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Pred. No. 6.1e-15;
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N
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/clone="258989"
/clone_lib="CITBI-E1"
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/organism."Homo sapiens"
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/dab_stage="Adult"

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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                 1 (bases 1 to 423)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
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TAG_SEQ=ATACGCGGTC"
100 c 111 g 101 t
                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
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RPCIII-126022.TJ RPCI-11 Homo sapiens genomic clone FPCI-11-126022,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hbefilgroup close are derived from the human BAC library kPC1-1). For BAC clones are derived from the human BAC library availability, please contact Pieter de Joseg (pieter*defong-med.buffalo.edu). Clones may be pirchased from BACPAC Resources (http://bacpac.med.buffalo.edu) or irom BACPAC Resources (http://bacpac.med.buffalo.edu.ordering) or irom http://www.tigr.org/tdb/humgen/bac.end_search/ser.etu_search.html
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Eukaryota: Motazoa; Chordata; Craniata; Verlebra: i. Buteleostomi:
Mammalia: eutheria: Primates; Catarthini: Hominidae: Homo.
1 (bases i Lo 581)
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Unpublished (1997)
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Coftect: Shaying Zhao, William Niefmd::, Mark Adams
Department of Eukaryotic Genomics
The institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, ML 22854
Tel: 301-838-0200
Fax: 301-838-0208
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6: Site_]:
RPCIII Human Male BAC Library"
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6.68; Score 214.2; DB ii
Best Local Similarity 81.28; Pred. No. 9.3e-15;
Matches 264; Conservative 0; Mismatches 53;
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/db_xref="GDB:7548357"
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/clone="RPCI-11-126022"
/clone_lib="RPCI-11"
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/clobe_lb="Morton Fetal Cochlea"
/tissue_type="cochlea"
/tissue_type="cochlea"
/do_stage="16-22 week fetus"
/do_stage="16-22 week fetus"
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/note="urgan: ear: Vector: pBluescript SK: Site_l: EcoRI:
Site_2: Xhol: Reference: Genomics 23, 42-50 (1994)
/do_pto_stage="16-22 week fetus"
/note="urgan: ear: Vector: pBluescript SK: Site_l: EcoRI:
Site_2: Xhol: Reference: Genomics 23, 42-50 (1994)
//do_pto_stage="16-22 week fetus"
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/do_pto
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Starayous a Metazoa; Chordata; Craniata; Vertebrata; Eutelecstomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
I (bases Lto 318)
Robertson, N.G., Khetarpal.U., Gutierrez-Espeleta, G.A., Bicher,F.R.
and Morton, N.G.,
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DNA sequencing and analyses were performed by National Institutes
                                                                                                                                                                                                                                                                          1186 GCTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGGT 1245
                                                                                                                      1126 AGTAAAGACTGGGTTTCAFCATGTFGGCCAGGTTGGTTTCGAACTCCTGACTGAGGTGA 1185
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This close is available royalty-free through LLNE; contact the This Consortium (info@image.llnl.gov) for further information. Plate: LLAM6168 row: G column: 15
                                      334 CTCCCGAGTAGCTGGGATTACAGGCGCCTGCCATCATGCTGGCTAATTTTGTATTTTT 275
                                                                                                                                                                                                                                                                                                                     214 TCTGCCCACCTTGGCCTCCCAAAGTGCTGGGTTACAGGCGTGAGCCACCACGCCCAGGC
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75 Francis Street, Harvard Medical School, Boston, MA 02115, 17
Tel: 617 738 6996
Fax: 617 738 6996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW02311; 338 bp mRNA linear EST di49606.yl Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2496822 5', mRNA sequence.
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Pred. No. 1.8e-14;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Best Local Similarity (81.9°
Matches 255: Conservative
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Fullyama.A., Hattori,M., Toyoda.A., Paylor,F.B., Yada,F.,
Fullyama.A., Hattori,M., Toyoda.A., Paylor,F.B., Yada,F.,
Direct Submission
Submitted (02-Aug. 2001) Asao Fullyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Screens From (GSC):
1-7-22 Suchiro-chou, Tsurumintu, Yokohama, Kunarawa 2 vg. 9645, Japan
(E-mail:chimpbes@gsc.riken.go.jp. 7RL:http://hdp.ysr.riken.go.jp/.
7e1381-45-503-9111, Fax:81-45-503-9170)
Glones are derived from the chimpuszee BAT (intery PIB Ihis BAC end
was generated during the RsD process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-068Pl9.R, genomic survey sequence.
AG075934
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Mammalia, Eutheria, Primates, Catarrhini, Haminidse: Pan.
PPPCTTTTTTTTTTTTTTTTGACACGGAGICTTGCTCTGTCACTCAGGGIGGAGIGCAGTGG 1013
                                                                                                                                1126 AUTAAAGACTGGGTTTCATCATGTTGGCCAGGTTGGTTTGGAACTTTGALCTGAAGGTGA 1185
                                                                                                                                                                                                                                                                    014 CAIGATOTOGACTOACTGTAACCTGGCGTGCGGGGTGAAGGGATTOTGGGGOTTGAGG 1073
                                                                                  257 CGIGAPCTIGGCTCACACCTTGCCTCCTGGGTTCAAGGATFCTCTCTGCTCAGC 198
                 197 CTCCCGAGTAGCTGAGATTACAGGTGCCCACCACCATGCCGGGCTAATTTTGTATTTTT 138
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/clone_lib="plB Chimpanzee Male EAV Library"
120 c 190 q 116 :
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Pred, No. 1e-14;
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/db_xref="taxon:9598"
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/sex="male"
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GSS 20-JUN-1998
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Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of human Bacterial Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: T7
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H50449 Tinear GSS 20-JUN-19 CIT-HSP HOMO Sapiens genomic clone 422022, DNA
347 TECTCECATITTAAAGATGAAGAAAGAGGCGGGCACAATGGCTAATGCCTGTAATCCC 406
                           646
                                                                                                                                                                                                                                                                                                                                                                                                                          467 GATAACATGGCAAAACCCTGTCTACAAAAAAAATACAAAATTAGATGGGTGGTGGTGG
                                                                                                                                                                                                                                                                                                                                                407 ACCACTITGGGAGGCTGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTG
                                                                                                                                                                                                                                                                                                                      587 GAGTCAAGTCTACACTGAGCCATGATTGGATCACTGCACTCCAGCCTGGGTAGACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other_OSSs: CIT HSP-422022.TP
Contact: Ung-Jin Kim
Calleth Genome Research Lab
Callifornia Institute of Technology
Division of Biology, MS 147.75, Pasadena, CA 91125,
Fax: 626 595 706
Fax: 626 595 4901
Email: ung%ash.tree.caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    767 AAAGAAAAAAAAAAGATGAAAGAGGCAGAAAGA 801
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Determination of clone end sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualitiers
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Clobes are derived from the human BAC library RPCI II. For BAC
Library availability, please contact Pieter de Jone
(pieter?dejong med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or trom
Research Genet cs (info@resgen.ens). BAC end search page:
http://www.tig.org/tdb/humgen/bac_erd_search/bac_end_search.html.
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Mammalia: Eutheria: Primates: Catasshins: Hono, Homo,
1 (bases 1 to 622)
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                                                                                                                                                                                      946 TCCATCCTTTCTTTTTTTTTTTTTTGACACGGAGTCTTGCTCTGLCACTCAGGCTGGAG 1005
                                                                                                                                                                                                                                                              1006 TGCAGTGGCATGATCTCGACTCACTGTAACCTCTGCCTCCCGGGGTTCAAGGGATTCTCCT 1065
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HindIII"
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Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
79712 Medical Center Dr., Rockville, Mp. 2085.
Tel: 301-838-0208
Fax: 301-838-0208
                                                          1 others
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332 GGOOGGGCGTCAGCCTAACTTTCAAATGACAA 355
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/db_xref-"GDB:7623762"
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Matches 267; Conservative
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178 c 103 g 218 t
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                                                                                                                                                                      Ouery Match 6.6%; Score 213.2; DB 17; Length 622; Best Local Similarity 73.2%; Pred. No. 1.1e-14; Matches 300; Conservative 0; Mismatches 108; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="kPC1-11-323E19"
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9, 2003, 12:19:31 ; Scarch time 174.697 Seconds (Without alignments) 5671.939 Million cell updates/sec
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GenCore version 5.1.5
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	15	267	8.3	45716	4	US-08-965-048-5	5
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U	15	257.8		246240	~	-08-724-	20,
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		250.2	7.7	21234	4	US-09-810-671-3	Sequence 3, Appli
		249.6	7.7	81001	4	US-09-750-580-1	'n

Sequence 10, Appll Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 13, Appl Sequence 2, Appl Sequence 17, Appl Sequence 3, Appl Sequence 3, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 67, A	NUCLEIC KINASE PROTEINS, AND USES	7.6; DB 4; Length 43950; tches 314; Indels 18; Gaps 5; tches 314; Indels 18; Gaps 5; tches 314; Indels 18; Gaps 5; AGCACTTGGGAGGCTGAGGCCAGAGA 434
US-09-734-673-3 US-08-257-963B-10 US-08-367-961B-10 US-08-367-941A-43 US-08-367-941A-43 US-09-975-223-2 US-09-128-155-17 US-09-128-155-17 US-09-657-44-7 US-09-657-44-7 US-09-637-44-7 US-09-637-44-7 US-09-630-35 US-09-630-35 US-09-630-35 US-09-630-35 US-09-630-35 US-09-630-35 US-08-975-08-35 US-08-975-08-35 US-08-975-08-35 US-08-975-08-35 US-08-832-88-67	ALIGNMENTS US/09735934A t al LATED HUMAN KINASE PROTEINS, ID MOLECULES ENCODING HUMAN EREOF 1 000-12-14 indows Version 4.0	Score 29     Pred: No
246.4 7.6 38564 4 243.4 7.5 7210 2 243.4 7.5 7210 4 243.4 7.5 22481 5 243.4 7.5 22481 5 243.4 7.5 22481 5 242.4 7.5 72604 4 242.4 7.5 72604 4 242.4 7.5 72604 4 240.2 7.4 14796 4 240.2 7.4 14796 4 240.2 7.4 14796 4 240.2 7.4 14796 4 240.2 7.4 14796 4 240.2 7.4 14796 4 240.2 7.4 14796 7 239 7.4 3507 2 238.8 7.4 3507 2	4A-3  6372468  1072468  110784710N:  11. Ji Jiayin e  110784710N:  110784710N:  110784710N:  110784710N:  110784710N:  1107847350  11078473	atch Sall Similarity Seal Similarity Seal Similarity Seal Similarity Seal Similarity CGCCGGGCACAATGCTAATGCCTC GGCCGGGCACAATGCTAATGCCTC GGCTGGGTTGGTTCTTCGGTC TCGCTGAGGTTGGTTTTGGGAC AAAAAAAAAA
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us-09-846-456-1.rni

: NAME/KEY: allele : LOCATION: 97122 : OTHER INFORMATION: 99:1442-224 : polymorphic base G or T	FEATURE:  SOUTHER INFORMATION: 5-129-144 : polymorphic base deletion of FEATURE:	: NAME/KEY: allele : LOCATION: 99098 : OTHER INFORMATION: 5-146-257 : polymorphic base A or C : FEATURE: NAME/KEY: allele	LOCATION: 99117 COTHER INFORMATION: 5-130-276 : polymorphic base A or 3 FEATURE: NAME/KEY: allele	LOCATION: 103806  ; OTHER INFORMATION: 5-131-395 : polymorphic base A or 1 ; FEATURE:   NAME/KEY: 411ele	CATION: 100340 CONTROL INSERTION: 5-133-375 : Polymorphic base insertion FEATURE: NAME/FEY: allele CONTROL: 108166	CTHER INFORMATION: 5-135-155 : polymorphic base insertion FEATURE:  NAME/KEY: allele : LCCATION: 108149 : CCATION: 108149	5 135-357 : polymorphic base	111ele 108471 RRATION: 5-136-174 : polymorphic base C or	FATURE:  NAME/KET: allele  LOCATION: 134134  OTHER INFORMATION: 5-140-120	: FEATURE:   NAME/KEY: allele   LOCATION: 134362   OTHER INFORMATION: 5-140-348 : polymorphic base insertion	FEATURE:  NAME/KE:  LOCATION: 134374  COTHER INFORMATION: 5-140-361 : polymorphic base insertion	FEATURE:   NAME/KEV: allele   COATION: 146328   OTHER INFORMATION: 5-143-84 : polymorphic base A or G	SEATONE: NAME/KED: allele COCATION: 146345 OTHER INFORMATION: 5-143-101 : polymorphic base A or C	FEATURE:  NAME/KEY: allele  LOCATION: 150329  OTHER INFORMATION: 5-145-24 : polymorphic base A or G	FEATURE: NAME/KRE: NAME/KRE: LOCATION: 160031 COTHER INFORMATION: 5-148-352 : polymorphic base G or T	NAME.
Db. 38021 CTACCTAATGCCCAGGAAAGCCTGAGAGGGGGGCTGCTATCAAGAAGCCCGCGAATAGAGAT 38080 Oy. 789 AGAGGGAAAGACTTTACGTAAATGCTGATGATGTGGTTGTGAAGTTGAAAGTGAAAA 848	38081 GACAAAATCAAGGCTGGAGAAATTAGGTCTTGACCTGAGATCATCGAGGGTTATTCTTG  849 CCCAATTTATGACCAAGGTTATTCTTTGACTGAGGGAAGGGGGTCGGCCCTTGGGGCC	DD - 88141 FOUTAGACACTGCTCAACACGTTGCATACATTCTCTTTCAGTTAAAAAAAA	959 CITGACACGAGICITGCICIGICACTAGACIGACIGACA GALCI CANTICA I I I I I I I I I I I I I I I I I I	Oy 1029 CTGTAACCTCTGCCTCCGGGTTCAAGGGATTCTGCTGGCTG	QY 1089 GCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	<ul> <li>99 1149 PIGGCCAGGTIGGTATCGAACTCCTGAGCTGAGCTGCCCACCITGGGCTGCCAAA 1208</li> <li>1014 HILL HILL HILLIHILIHII   111   1</li></ul>	Ub 38492 GTGCTGAGATTGCAGGCATCACCACCACCATCATGTATA: 38537	RESULT: 2 US-19-145 BB2 1 : Sequence 1, Application US/09345882 : Patent No. 6399373	GENERAL INFORMATION: APPLICANT: BOUGUELEET, LYGIG TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOSTASTOMA RINDING PROTEIN (RBP-7) TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.	: FILE REFERÊNCE: GENEET USIA : CURRENT APPLICATION NUMBER: US/09/345,882 : CURRENT FILING DATE: 1999-06-30 : PRIOR APPLICATION NUMBER: US 60/091,*15	PRIOR FILING DATE: 1998-06-30  PRIOR APPLICATION NUMBER: US 60/111,909  PRIOR FILING DATE: 1998-12-10  NUMBER OF SEQ ID NOS: 140	: SEQ I NO 1 : EMCTH: 162450 : TYPE: DNA		5.124-2/3 : POLYMOLPHIC BASE A	: polymorphic base A of .	COTHER INFORMATION: 99-1437-323 : POLYMOIPHIC DASE A G: G : FEATURE: FEATURE: NAMECKEY: allele : LOCATION: 93714 : CTHER INFORMATION: 5-128-60 : polymoiphic base deletion G: G:

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OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                           NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymo
                                             108130
                                                                                                                                                                          108177
             FEATURE:
NAME/KEY: allele
LOCATION: 108084..10
OTHER INFORMATION: p
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FEATURE:
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                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 90819...90865
OTHER INFORMATION: COMplement polymorphic fraqment 99-1437-325 SE2 IE70
                                                                                                                                                                                                         49-1437-325 SEQ ID49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEC 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 97099, 97145
OTHER INFORMATION: polymorphic fragment, 99:1442-224 SEC 1D7.
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LOCATION: 99075..99121
CYBER INFORMATION: polymorphic fragment 5-1-0, 257 SEQ (10-)
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LOCATION: 72771..72817
OTHER INFORMATION: polymorphic tragment 5-124-273 SEC IDS1
                                                                                                                                            7.007
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130 276 SEy
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OTHER INFORMATION: POLYMOFPHIC fraqment 5-129-144 SEC
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(1)
(2)
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GIMER INFORMATION: complement polymorphic fraqment
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LOCATION: 57130...57177
OTHER INFORMATION: Polymorphic fragment, 5-129-144
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OTHER INFORMATION: polymorphic fragment 5 130 276
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                                             NAME/KEY: allele
LOCATION: 88050..88096
COTHER THFORMATION: polymorphic fraqment 5 127..
PSTICKE:
NAME/KEY: allele
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LOCATION: 93690..94736
CTHEK INFORMATION: polymorphic fragment 5-128
                                                                                                                                          OTHER INFORMATION: polymorphic fragment 5-127
FEATURE:
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LOCATION: 106918..106966
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LOCALION: 97099.97145
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LOCATION: 99075..99121
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LOCATION: 103783.
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27476 TCA--TGAGGTCAAGAGTTGAGACCATCTGGCCAATATAGTGAAACCCCGCCTCTACT 27533 27593 27714 AAAAAAGTALIGTEGIAGFFFFFFFFFFFFFGCAAGCAICTTTAAFGTAGAATAA 27773 28071 27416 GGCTGGGGGTAGTGCTCACGCCTATAATCCAGCACTCTGGGAGGCGGGGGAGGCAGGAGA 27475 1081 549 606 550 TTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCCAGGGAGTCAAGTCTACACTGAGCCAT 609 TCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATAACATGGCAAAACCCTGTCTCTAGA 494 375 GGCCGGCCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCCAGAGGA 434 790 GAGGCAGAAAGACTTTACGTAAATTGCTCATCATGTGGTTGTCAAGTTTGACCCCAAAAC 27834 TAIGTGTJAFGTTGTTGTAAGCACAGATATGTCATTTAATGTTCATGATAGCAGTATG 850 CCAATTIATTGACCAAGGITATTGTTTGACTGAGGCGAAGGGGGTCCGCTCCTGGGCCT 970 Indacadadrenraciererereacteaderecadiceacteacteacteac 1030 TGIAACC1CTGCCCCCCCCCCCTCAACCGATTCTCCTGCCTCAGCCTC-----CTGAG 495 AAAAAAATACA --- - AAAATTAGATGGGTGTGGTGGCATGCACCTGTGGTCCCAGCTAC Length 162450; .. 8: LOCATION: 108127..108177 OTHER INFORMATION: FG:ymorphic fragment 5-135-198 SEQ ID60 PEATURE: SEQ ID38 SEQ ID39 Indels Ouery Match 9.1%; Score 292.6; DB 4; Rest Local Similarity 61.2%; Pred. No. 5.2e-62; Matches 564; Conservative 0; Mismatches 339; polymorphic fragment 5-135-155 polymorphic tragment 5-135-155 polymorphic fragment 5-135-198

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10-510-173 : variable motif ATTTA or TTTTT
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OTHER INFORMATION: 10·509·284
NAME/KEY: allele
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                                                                                                                                           NAME/KEY: exon
LOCATION: 16567...16667
OTHER INFORMATION: exon 12
                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 16775..16945
OTHER INFORMATION: exon 13
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: exon 14 NAME/KEY: misc_feature LOCATION: 17555..26674
                                                           OTHER INFORMATION: exon 10
                                                                                                     LOCATION: 13308..13429
OTHER INFORMATION: exon 11
OTHER INFORMATION: exon 9
                                                                             NAME/KEY: exon
LOCATION: 13308..13429
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LOCATION: 17063..17554
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: 2341
OTHER INFORMATION:
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LOCATION: 4062
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LOCATION: 1128
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LOCATION: 1182
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LOCATION: 2048
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LOCATION: 2832
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LOCATION: 2947
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LOCATION: 4109
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LOCALION: 4170
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Buimenfeld, Marta
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Chumakov, 11ya
APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKENS DERIVED FROM GENOM: ERCICUS
TITLE OF INVENTION: GENES INVOLVED IN ARACHICONIC ACID METARGLISM
FILE REFERENCE: 2000-08-16
CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-02-11
PRIOR FILING DATE: 1099-03-07
PRIOR APPLICATION NUMBER: US 60/133.206
PRIOR APPLICATION NUMBER: US 60/133.206
PRIOR APPLICATION NUMBER: US 60/133.207
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-13
SPRIOR FILING DATE: 1999-02-12
NUMBER OF SRU ID NOS: 1304
SSOFTWARE: PALECL, pm
28132 ATTGCAGGCACCGCCACCCCACCTGGCTAAATTTTGTATTTTTGGTAGAATGGGGTT 28191
                                                           28192 TEGGGAGGTGGGCGGGGTGTTCTCGGACCTCAAGGGGTTGCTGGGCTGTGAGCC28251
                                                                                                                                               28252 CECCCAAAGTGCTGGGATTACAGGTATGAGGCACTGEGCTGGCCGGAGAGGCTGTTTTC 28311
                                                                                                                         1201 CTGCCAAAGTGCTGGGATTACAGGCATGAGGCACTGGGCCCAAGGCTGAGTCATGGGTTT 1269
                                       1141 TCATCATGTTGGCCAGGTTGGATTTCGAACTCCTGACCTGAGGTGAGTTGCCTAGTTTGGC 1200
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loCalion: 1123.33133
OTHER INCOMMATION: 5'requiatory region
NAME/KEY: EXCH
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Patent No. 6432648
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OTHER INFORMATION: exon 7
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IOCATION: 5758..5880
OTHER INFORMATION: exon 4
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OTHER INFORMATION: exon 1
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LOCATION: 6349..6509
OTHER INFCRMATION: exon
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OTHER INFORMATION: exon
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LOCATION: 5996..6099
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LOCATION: 5552..5633
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Zianqhe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEAS KENTION: ISOLAFED HUMAN PROTEASE PROTEINS, FENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, A PENTION: ISES THEREOF

Length, 20674;

DB 4;

Scure 285.4;

8.88;

Onery Match

9 16078 TGAAACCCCGGCTCTACTAAAAATA-GGAAAAGTTACCAAGGTGTGGCGGGCGGCCCG 16020 15541 15481 15421 15900 CTCAAAAAAAAAAAACCAATTGAGGGATGCGTGGTCGGTGACTCATGCCTGTAATCCCA :5841 15781 15780 ICTCTATITAAAAAATTAAAAAAATAAATAATTTAGGAATGCGTAATCCTATTGCGGG \S721 15601 1058 1110 1170 15720 ACAGAATTACAAGIGICIGGGITATAATGIGGGGAATAAGTCATGGATTICCAGIGICAC 15661 417 GASGCFGASGCFAGAGGATGGCTTGAGCTCCAGAGTTTGAGACCAGGCTGGATAACATGG 476 TTTAAAGATGAAGAAACAGCCGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGG 416 30; Gaps 477 CAAAACCTTGTCTGCAAAAAAAAIACAAAATTAGATGGGTGGGTGCCATGCACCTG 763 GAAAAAAAAAAAAAAAGATGAAACAGAGGCAGAAAGACTTTACGTAAATIGCTCATCA 15660 AGCTGAGAGGGCTCCCACAAAGGTTATCTCAGTCCACTCATTTTGCAGTGGATATGGGG 597 TACACTGAGCCATGATTGGATCACTGCACTCCAGCCTGGGTAGACAGAGCAAGACCTGT 823 TGTGGTTGTCRAGTTTGACCCCAAAACCCAATTTATTGACCAAGGTTATTCTTTGACTGA 883 GGCAAGGGGGTCCGGTTCCTGGGCCTTGGGCTTTAGAAAGCTCATCTCTGGCCTT----939 TCTGAGATCCATCCTTTCTTTAT:TTTCTTGACACGGAGTCTTGCTCTGACTCAG 1059 TTCTCCTGCCTCAGCCTC ----- CTGAGATAACAGGCGCCCGCCACCACATCTGGGT AATTI TIGITATI LITAGI AAASACTGGGTTTCATCATGTTGGCCAGGTTGGTTTCGAACT 15360 CCTGGCCTCAGGTGATCTGCCCACCTTGAAGTGCTGGGA 15314 1171 CCTGACCTGAGGTGAGCTGCCCACCTTGGCGTCCCAAAGTGCTGGGA 1217 Indels Pred. No. 1.2e-60; ; Mismatches 301; Sequence 3, Application US/09797906
Patent No. 6242188
GENERAL INFORMATION
APPLICANT: Zianghe YAN, Karen A. KET
TITLE OF INVENTION: USGLAFED HUBAN E;
TITLE OF INVENTION: UNCLEIC ACID MOI
TITLE OF INVENTION: USES THEREOF ; 62.78; Best Local Similarity 62.7 Matches 556; Conservative US-09-797-906-3 357 657 1111 9 a ò 3 a ô ďЗ g ć 3 ć ac ô g a à 3 ŝ ò 5 q ò a ò ŝ ò ŝ ô

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Best Local Similarity 61.5%; Pred. No. 1.4e-58;
Matches 553; Conservative 0; Mismatches 3.28;
FILE REFERENCE: CL001151CIP
CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)...(84495)
OTHER INFORMATION: n - A,T,C or G
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APPLICANT: Zianqhe YaN, karen A. KETCHUM, Valentina DIFPANCESCO, Ellen M. BEA TITLE DE INVENTION: 1801.ATED HUMAN PROTEASE PROTEINS, TITLE DE INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, TITLE DE INVENTION: USES THEREOF FILE REFERENCE: CLOONIS-CLOOR CURRENT APPLICATION NUMBER: US/09/797,906
CURRENT FILING DATE: 2601-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                           885 CAAGGGGGTCGGCTGTCTGGGCTTTGGGGTTTAGAAAGCTCATCTCTGGCCTTTGTGAG 944
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61.1%; Pred. No. 2.5e-58;
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OTHER INFORMATION: n \rightarrow A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09797906
Patent No. 6329188
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APPLICANT: Zianghe
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Sequence 3. Application US/09817180
Patent No. 6440584
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLE:C
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001183
CURRENT APPLICATION NUMBER: US/09/817,180
CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ 1D NOS: 4
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                                                                                                          35138 FITTATITATITATITATITATITAGAGAIGAGUCHGICHCHGICAGAGAGGG 35079
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Pred. No. 2.4er57;
0; Mismatches 287;
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US-09-817-180-3
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APPLICANT: Bougueleret, Lydie
TITLE DE INVENTIEM: A NUCLEIC ACID ENCODING A RETINOBLASIOMA BINDING PROTEIN (
TITLE DE INVENTION: A NUCLEIC ACID ENCOPPIC MARKERS ASSOCIATED WITH SALD NUCLEIC ACID
FILE REFERENCE: GENSET.031A
                                                                         14750 AAACAAAGGAAUTTGTGTTGTCGTGTAATTAAATGAAAATACTAGGAAGTGAAATAAIA 14809
                                                                                                                                                  ------CCTCCAAIGGAAAIGCIAGAAAGCAGA 14836
                                                                                                                                                                                                              14690 AAAACACAACAAAAATCTATTTTGAAAGAGATGAGAGTGAGCCATATAACTTGTTT 14749
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CURRENT FILING DATE: 1995-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-16-30
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-345-882-1/c
; Sequence 1, Application US/09345882
; Patent No. 6399373
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OTHER INFORMATION: 5-127-261
FEATURE:
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FEATURE:
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99-1437-325	5-128-60	99-1442-224	5-129-144	5-130-257	5-130-276	5-131-395	5-133-375	5-135-155	5-135-198	5-135-357	5-136-174	5-140-120	5-140-348	5-140-361	5-143-84	5-143-101	5-145-24
NAME/KEY: allele LOCATION: 90842 OTHER INFORMATION:	FEATURE: NAME/KEY: allelc LOCATION: 93714 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 97122 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 97152 GIAGRE INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 99098 OTHER INFORMATION: FEATURE:	NAME/KEY: allele LOCATION: 99117 OTHER INFORMATION: FFATURE:	NAME/KEY: allele LOCATION: 103806 OTHER INFORMATION: FEATURE:	NAME/KEY: allele LOCATION: 106940 OTHER INFORMATION: FEATURE:	NAME/KEY: allele LOCATION: 108106 OTHER INFORMATION:	FEATORE: NAME/KEY: allele LOCATION: 108149 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LCKTATION: 108308 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 108471 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 134134 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 134362 OTHER INFORMATION:	Fraidre: NAME/KEY: allele LOCATION: 134374 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 146328 OTHER INFORMATION:	REATORE: NAME/KEY: allele LOCATION: 146345 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 150329 OTHER INFORMATION: FEATURE: NAME/KEY: allele

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90819..90865
RMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
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RMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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97099..97145
NRMATION: polymorphic fragment 99-1442-224 SEQ ID50
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72771...72817
NRMATION: polymorphic fragment 5-124-273 SEQ ID30
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97130. 97177
08MATION: polymorphic fragment 5-129-144 SEQ ID33
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88050..88096
NRMATION: polymorphic fragment 5-127-261 SEQ ID31
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88050..88096
RMATION: polymorphic fragment 5-127-261 SEQ ID52
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99094...99140
NRMATION: polymorphic fragment 5-130-276 SEQ ID35
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99075..99121
DRMATTON: polymorphic fragment 5-130-257 SEQ ID55
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99094...99140
NRMATION: polymorphic fragment 5-130-276 SEQ ID56
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103783...103828
RMATION: polymorphic fragment 5-131-395 SEQ ID36
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72771, 72817
RHATION: polymorphic fragment 5-124-273 SEQ ID51
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97136..97177
8MATION: polymorphic fragment 5-129-144 SEQ ID54
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99075..99121
RMATION: polymorphic fragment 5-130-257 SEQ ID34
160031
RMATION: 5-148-352 : polymorphic base G or
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93690. 93736
RMATION: polymorphic fragment 5-128-60 SEQ ID32
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RMATION: polymorphic tragment 5-128-60 SEQ ID53
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LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEC 1060
INFORMATION: polymorphic tragment 5-131-395 SEQ 1D57
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61.3%; Pred. No. 8.3e-57;
ative 0; Mismatches 324;
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OTHER INFORMATION: polymorphic fragment 5-135-198
                                                                                                                     LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133:375
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N: polymorphic fragment 5-135:155
                                                LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment
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LOCATION: 108127..108177
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Best Local Similarity
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LOCATION: 106918.
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GENERAL INFORMATION:
APPLICANT: LI, Jiayin et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
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                                                     27519 TICACTAIAITGGCGAGGATGGTCTCAATCTCTTGACCTCA--TGATCTGCCTGGGTGCTGG
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61.3%; Pred. No. 5.5e-57;
tive 0; Mismatches 318;
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CURRENT APPLICATION NUMBER: US/09/735,934A
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 4
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SEO ID NO 3
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Best Local Similarity 61.3%
Matches 552; Conservative
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FILE REFERENCE: 4121-108
FILE REFERENCE: 4121-108
FURRENT APPLICATION NUMBER: US/09/341,587
FURRENT FILING DATE: 1999-08-31
FARLIER APPLICATION NUMBER: PCT/DE98/U6096
NUMBER OF SEQ. 1D NOS: 12
SCHTWARE: Patentin Ver. 2.1
SEQ ID NO
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US-09-341-587-7
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Sequence 3, Application US/U9734673
Patent No. 6410294
GENERAL INFORMATION:
ADPLICANT: GUEGIER, Karl et al
TITLE OF INVENTION: 1SOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION:
FILE REFERENCE: CL001020
CURRENT APPLICATION NUMBER: US/09/734,673
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18980 AGGTTGTGGTGAACTATGATAGCGCCAGTGCACTCCAGCTTGTGGA-ACAAAACGAGACC 19038
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                                 Length 38564;
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Pred. No. 3.2e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: n = 4
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LOCATION: (1). (38564
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Best Local Similarity

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    34; Gaps
                                                                                                                               495 AAAAAAATACAAAATTAGATGGGTGTGGCATGTACCTGTGCTCCCAGTTACTTGGG
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Sequence 1, Application US/09750580
Patent No. 6455280
GENERAL INFORMATION:
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APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Balbets Reed, Dana
APPLICANT: Balter-Cid, Luisa
FILE REFERENCE:
FILE REFERENCE:
B9.1022.C1P
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT APPLICATION NUMBER: US/09/750,580
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: PCT/1B00/0101
PRIOR APPLICATION NUMBER: PCT/1B09/02058
PRIOR APPLICATION NUMBER: PCT/1B99/02058
PRIOR APPLICATION NUMBER: US/09/099
PRIOR FILING DATE: 1999-12-21
PRIOR PELLING DATE: 1999-12-21
PRIOR FILING DATE: 1999-10-22
PRIOR FILING DATE: 1999-10-25
PRIOR FILING DATE: 1999-10-25
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                                                                     Dumas Milne Edwards, Jean-Baptiste
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NAME/KEY: primer_bisd
LOCATION: 929.949
LOCATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
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OTHER INFORMATION: exon 4
NAME/EXP: misc_teat.ne
LACATION: 15969...17969
OTHER INFORMATION: 3'requiatory region
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NAME/KEY: Alicle
LOCATION: 12347
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                                                                                               Duclert, Aymeric
Denison, Blake
Bour, Barbara
Bihain, Bernard
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OTHER INFOHMATION: CKGG 2
NAME/MES: EKOD
LOCATION: 13641., 14752
OTHER INFORMATION: CKGG 3
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LOCATION: 10946..12946
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LOCATION: 77058
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LOCATION: 12947
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APPLICANT:
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LOCATION: 45443..45461 OTHER INFORMATION: 20-842-115.mis compterent OTHER INFORMATION: 20-853-415.mis complement. complement. complement UCCATION: 12348..12366 OTHER INFORMATION: 17-42-319.mis complement NAME/KEY: Primer\_blind LOCATION: 15222..15240 OTHER INFORMATION: 17-41-250 mis complement LOCATION: 77166..77185
OTHER INFORMATION: 20-853.rp complement
NAME/KEY: primer\_bind NAME/KEY: primer\_bind LOCATION: 42572..42591 OTHER INFORMATION: 20-841.rp complement OTHER INFORMATION: 17-41.pu
NAME/KEY: primer\_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement.
NAME/KEY: primer\_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu LOCATION: 12581..12603 OTHER INFORMATION: 17-42.rp complement OTHER INFORMATION: 20-828-311.probe OTHER INFORMATION: 17-42-319.probe NAME/KEY: misc\_binding OTHER INFORMATION: 20-828-311.mis NAME/KEY: primer\_bind OTHER INFORMATION: 20-841-149.mis NAME/KEY: primer\_bind COCATION: 1220..1238
OTHER INFORMATION: 26-828-311.mis
NAME/KEY: primer bind
LOCATION: 1240..1258 OTHER INFORMATION: 20-841-149.mis NAME/KEY: primer\_bind LXCATION: 42219..42237 IXCALLON: 45423..4544,
OTHER INFORMATION: 20.842-115.mis
NAME/KEY: primer\_bind OTHER INFORMATION: 20-853-415.mis NAME/KEY: primer\_bind OTHER INFORMATION: 17-42-319.mis NAME/KEY: primer\_bind UTHER INFORMATION: 20-842.rp NAME/KEY: primer\_bind LACATION: 76644..76664 OTHER INFORMATION: 20-842.pu NAME/KEY: primer\_bind LOCATION: 45863..45883 OTHER INFORMATION: 20-853.pu nd LOCATION: 12029...12050 OTHER INFORMATION: 17-42. NAME/KEY: primer N:--NAME/KEY: misc\_binding 14992..15012 NAME/KEY: primer\_bind LOCATION: 45328..45347 NAME/KEY: primer\_bind LOCATION: 15242..15260 LOCATION: 77059..77077 misc\_binding NAME/KEY: primer\_bind LOCATION: 77166..77185 12328..12346 NAME/KEY: primer\_bind LCA'ATION: 42199..42217 primer\_bind 45423..45441 primer\_bind primer\_bind 77039. NAME/KEY: LOCATION: LOCATION: LOCATION:

6 53637 IGGATGGTATTCCAAAGCACCAAGGAAACCACTTTTTTACCTTGGAAATAAGGTCTTA 53578 53517 GCAGAATUAGAAAAQAATTGCAGGAGAAACTCACAGTGGAAAGAGCTTTGGACCAGAGAA 53458 1109 CTAATITIT ---GRATITITASTAAAGACTGGGTTTCATCATGTTGGCCAGGTTGGTTT 1164 597 418 AGGCTGAGGCCAGAGGATCGCTTGAGCTCCAGAGTTTGAGACCAGCCTGGATAACATGGC 477 775 AAACAAGATGAAAGAGAGAGAAAGACTTTACGTAAATTGCTCATCATGTGGTTGTCAA 834 38; Gaps 53874 GAAACCCTGTCTCTAC--TAAAATACAAAAATTAGCTGGGGGTGGT-GCTCACCTGT GGTCCCAGCTACTTGGGAGGCTAAAGGTGGGAGGATCGCTTGAGCCCAGGGAGTCAAGTCT 598 ACACTGAGCCATGATTGGATCA - - CTGCACTCCAGCCTGGGTAGACAGAGCAAGACCTG 53577 AGAGAGITACACITACATATATACAAAGGACATATGAATAACAAACACCAAAICCTAA 835 GTTTGACCCCAAAACCAAFTTA---- --TTGACCAAGGTTATTCTTTGACTGAGGCAA 53457 TCAGGAACGCAGAGTTCTAATTCCAGCTTTCTCAGGGAAATTGCATGACTCTAGGCAAAC 358 TIAAAGAIGAAGAAACAGGCCGGCCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGG 888 GGGGTCCCCTCTCTGGCCTTGGCCTTTAGAAAGCTCATCTCTGGCCTTTCTGAGATC 997 AGGCTGGAGTGCAGTGGCATGTCTCGACTCACTGTAACCTCTGCCTCCCGGGTTCAAGC 1057 GATTCTCCTGCTGAGCCT- -----CCTGAGATAACAGGCGCCGCCACATCTGG 478 AAAACCCTG1CTCTACAAAAAAAAAAAATTAGATGGGTGTGGCATGCACCTGT 948 -- ---- CATCCCTTCTTTTTTTTTTTTTGACACGGAGTCTTGCTCTGTCACTC Length 81001; Indels 0; Mismatches 309; DB 4; Score 267.6; DB 4 Pred. No. 5.8e-56; LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/CKI misc\_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/CKI misc\_binding
LOCATION: 45454
OTHER INFORMATION: 20-842-115.probe NAME/KEY: misc\_binding LCCATION: 77046...77070 OTHER INFORMATION: 20-853-415.probe US-09-750-580-1 8.3%; Similarity 62.6%; Conservative Query Match Best Local Simi Matches 581; 538 959 a ä a Š ò Q C ć 9 ò q 9 ò 5 õ a ŝ Š 3 ŝ a 3 ô â Š ò ŝ ŝ

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507 AAATTAGATGGGTGTGGTGGCATGCCATCTGGTCTTGGTAGGTGTAAGGTG 566 1111111 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 1
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1165 GAACTCCTGACCTGAGGTGAGCTGCCCACCTTGGCCTCCCAAAG1GCTGGGAI.ACAGG 1224
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APPLICANT: Ereimer, Nelson
APPLICANT: Branch APPLICATION: METHODS AND COMPOSITIONS FOR THE LIAGON S:S AND
APPLICATION: TREATMENT OF NEUROPSYCHIATRIC DISCREERS
FILE REFRENCE: 7853-093
CURRENT APPLICATION NUMBER: US/08/965,648
CURRENT FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE PALENTIN VEr. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 45718;
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Pred. No. 6.2e.56;
                                                                                                                                                                                         Ob 53059 CATGAGGGACCGCACCGGCCCGGTTC 54072
                                                                                                                                                 1225 CATGAGGGACTGGGGCCCAGGTCG 1252
                                                                                                                                                                                                                                                                                                                                                                                                                  : Sequence 5, Application US/08965048
: Patent No. 6323244
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.3%;
Matches 571; Conservative
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US-08-965-048-5
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                                                                 1113 TITTTGTAFTTTTAGTAAAGACTGGGTTTCATCATGTTGGCCAGGTTGGTATTGGAACTCC
                                                                                                                                                                     CTCCTGCCTGAGCCTC - - - - - - - CTGAGATAACAGGCGCCGCCACCACATGTGGCTAA
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APPLICANT: Chen, Hong
APPLICANT: Freimer, Nelson
TITLE OF INVENTION: HEATHENT OF NEUMOPSYCHIATRIC DISORDERS
TITLE OF INVENTION: HEATHENT OF NEUMOPSYCHIATRIC DISORDERS
TITLE REPERENCE: 1853-093
CURRENT APPLICATION NUMBER: US/08/965,048
CURRENT FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 8
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Pred, No. 6.2e-56;
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; Patent No. 6323244
; GENERAL INFORMATION:
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Best Local Similarity 61.3
Matches 571; Conservative
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US-08-965-048 6
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                                                                                                                                                                                                     GIGAGCCICCCIGATCAGAAGIAGGATATIIICAAGAAAAGGAATAAAAGGIGIGCICCA 7891
                                                                                                                                                                                                                                   941 IGAGATOCATOCOTTCTTTTATTTTTCTTGACACGGAUICITGCTCTGTCACICAGGC 1000
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                                                                                    7712 GGGTGTAFGTTGTGTGCGAGCTCTCAAGTGCCTTGTTAGAAIGAGCTGTTTGGAGT 7771
                                                                                                                                             7772 FGACCATGGAGATGGCTTCACATGCCCTGGAGGCATGGTGGACGATGAGGACTTAGGAA 7831
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                                                                                                                889 GGGGTCCGCTCTCCTGGGCCTTGGGCTTT-- --- AGAAAGATCATCTCTGGCCTTTTC 940
                                                       1001 TGGAGIGCAGIGGCATGATCTCGACTCACIGTAGCCTCTGCCTCGCGGTICAGCGAIT
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APPLICANT: Choo, Kong-Hong Andy
APPLICANT: Use Sart, Desiree
APPLICANT: Du Sart, Desiree
CURRENT APPLICATION UNDRER: US/09/078,294
CURRENT FILIG DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
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: Sequence 12, Application US/09078294
: Patent No. 6265211
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TYPE: DNA
: ORGANISM: BAC-F2 contig 8
CS:09-078-294 12
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1258 TCATTATACATITGTCCAAATCTACAGAATGTACAACACCAAAGCTTGGGTGATAATGAG 1199
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                                                                                                                                                                                                                                                        714
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                                                                                   GCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGGCCCAGGGAGTCAAGTCTACACTGA
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TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 33
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; Sequence 20, Application US/08724394A
; Patent No. 5872237
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APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
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APPLICANT: Kronmal, Gredory
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
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SFATE: CA
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Db 172582 GCGGGGGCCAATGGCCACGCCTGTAATGCCACCTTGGGA-GCTGAGGGGGGGAGC 172524
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Pred. No. 2.7e-53;
0; Mismatches 412; indexs 30;
                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
SUSTEM: PC-DOS/MS-DOS
SUFTWARE: Patentin Release #1.0, Version #1.36
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                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 017957-030100 TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
                                                                                                                                   APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
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not relevant
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LENGTH: 246240 base pairs
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Best Local Similarity 61.4%;
Matches 545; Conservative (
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LOCAFION: 1..246240
CTHER INFORMATION: /note
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,1
                                                                                                                 CURRENT APPLICATION DATA:
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STRANDEDNESS: not r
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GenCore version 5.1.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli		Sequence 23, Appl		sequence 137, App	Sequence 139, App	Sequence 140, App	Sequence 141, App	Sequence 142, App	Sequence 143, App	Sequence 144, App	145,	Seguence 146,	Sequence 148,	149,	Sequence 152, App	Sequence 153, App	Sequence 154, App	Sequence 155, App
ID	US-09-984-827-3	US-09-846-456-1	US-09-984-827-23	US-09-846-456-3	US-09-984-827 137	US-09-984-827-139	US-09-984-827-14(	US-09-984-827-141	US-09-984-827-142	US-09-984-827-143	US-09-984-827-144	US-09-984-827-14	US-09-984-827-146	US-09-984-827-148	US-09-984-827-149	US-09-984-827-152	US-09-984-827-15	US-09-984-827-154	US-09-984-827-155
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% Query Match	100.0	100.0	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5
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                                                                          GGCTGCCGGGAACGTGGACTAGAGAGTCTGCGGCGCAGCCCCGAGCCCAGCCCTTCCCGC
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                             AAAGGAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTT
AAGTGCTCGGTTTCGGGGGCTTTGATCCGGGGCCCCCACATCTTTACCACTT 3231
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Duverger, Nicolas
Brewer, Bryan
Remaley, Alan
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APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
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TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modi
TITLE OF INVENTION: Activity and Therapeutic Uses
FILE REFERENCE: 3806.0505
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT FILING DATE: 2001.05.02
PRIOR APPLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 2000-05-02
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SOFTWARE: Patentin version 3.0
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09   361 AAGATGAAGAAGCCGGGCACAATGGCTAATGCCTGTAATCCCAGCACTTTGGGAGG 420   11111111111111111111111111111111111	Oy         541 CCCAGGTATTIGGAGGTATAGGTGGAGGATGGCTTGAGGGAGTCAAGTCTACA 600           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY         661 AAAAAAGAAATGAAAGAAAGAAAGAAAGAGAGGAGGAGGA	QY         781 GATGAAACAGAGCGAAAGACTTTACGTAAATTGCTCATCATGGTTGTCAASTTTGA 840           111111111111111111111111111111111111	QY         901 CCTGGGCCTFGGGCTTTGGAAAGCTCATCTGGCCTTTCTGTTT 960	QY         1021         TCGACTCACTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGA         1080           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         1141 TCATCATGTTGGCCAGGTTGGTTCGAACTCCTGAGGTGAGCTGCCCACCTTGGC 1200           DA         [HILLI] [HILLI] [HILLI] [HILLI] [HILLI] [HILLI] [HILLI]           Db         1141 TCATCATGTTGGCGTTGGGTTTGGACTCCTGAGCTGAGC	CTAMUSGCAAACAGTCCATGGTGCAAAGGGGCCATGCCACCAGAGTTATGAGTACCTGG	Oy 1381 TTCTANGGCTCTGCTGAGTGTTGANGAACCACTGATGTGAGTACCTGGGCTTGAGCC 1440
CGGTTCTCAGGGCGCTTTGCTCTTGTTTTTCCCCGGTTCTGTTTTCTCCCCGGGGGG	113. GGTCTCCAGIGACTIACTICGCCGTATICTTTGTTTGGAGGCCAAGGAGGGGGGGGGG	US 09 984 827 23 Sequence 23, Application US/09984827 Sequence 23, Application US/09984827 GENERAL INFORMATION: APPLICANT: DENEELE, PATRICE APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE APPLICANT: ARROULD-REGUIGNE, ISABELE APPLICANT: DUVERGER, NICOLAS	APPLICANT: CAMBIEN, FRANCIS TITLE OF INVENTION: DETECTION METHODS AND TITS THEREFORE TITLE OF INVENTION: DETECTION METHODS AND TITS THEREFORE FILE REFERENCE: 03806.0522-00000 CURRENT APPLICATION NUMBER: 05/09/984,827 CURRENT FILING DATE: 2002-04-01 PRIOR APPLICATION NUMBER: 60/254,108 PRIOR FILING DATE: 2000-12-11	PRIOR FILING DATE: 2000-10-31  PRIOR FILING DATE: 2000-10-31  NUMBER OF SEQ ID NOS: 161  SOPTWARE: Patentin Ver. 2.1  SEQ ID NO 23  LENGTH: 2893  TYPE: DNA  SOPTWARE: Homo Sapkers	Query Match 89.5%; Score 2893; DB 9; Length 2893; Best Local Similarity 100.0%; Pred. No. 0; Manatches 2893; Conservative 0; Mismatches 0; Indels U. Gaps 0; AcadeGCATGCTGTAATCTCAATCACTGGAAGATGATGAATGA 60	ACAGGGCALGGTGGCAGGTGCCTGTAATCTCGSSAGGTGGGGGGTTGGAATGAATGAAAGGTGGGAGGTTGGAATTGGAGTGGAGGTTGGAATGAAGGTGGAAAGGTGGAAACTCCTGTGTGCAGTTGGAGTGGAGGTGGAAGGTGGAAGGTGGAAGTTTGGCAGATGGCAGTTGGAGTCCAGGCCTGGGCAACAAAAAAAGAAGGAGCGAGTTTTGGTGGTCCAGCTTCCAATTTTGGTGGTCGAGCTGCAGTAGGAAGAAGAAGAAGAAGAAGAAGAATTTTGGTGGTCCTAACTTCAAATAGGTAGAGAAGAAGAAGAAGAAGAAGAAGAATTTTGGTGG	AAAAAAAAGGCCGGGGGGGCGCCTCCAAATAGCTGGGGAAAAAAGGAAGAAGGGGGGGG	24. ITTAATAACAUTCIUTGUTITTATAACATCATUGUCAAGGGCTCAAAGGTTTCAACA 360 301 AAGTICACTTICAGAAACCCUTTGAGGAAGACAGAATACATCTTCTCCATTTA 360 111111111111111111111111111111111111

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APPLICANT:
Duverger, Nicolas
APPLICANT:
Brewer, Bryan
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Bromaley, Alan
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APPLICANT:
Bromaley, Alan
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Fromaley, Alan
TITLE OF INVENTION:
Requistory Nucleic Acid for the ABC1 Gene, Molecules Modif
TITLE OF INVENTION:
Arctivity and Therapeutic Uses
TITLE OF INVENTION:
Arctivity and Therapeutic Uses
CURRENT APPLICATION NUMBER: US/C9/846,456
CURRENT FILING LATE: 2001-05·02
PRIOR FILING DATE: 2001-05·02
PRIOR FILING DATE: 2001-05·02
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Sequence 3. Application US/09846456
Patent No. US20020146792A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
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Duverger, Nicolas
Brewer, Bryan
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APPLICANT: Prades, Catherine
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APPLICANT: Naudin, Laurent
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APPLICANT:
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150 150	1 IGCAGGIGGIGGAGTICTGGAATATGATGGAGCTGGAGGTGGGAGAGAAGTAGGCTTG 1	560 560
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222	21 CCTGGGGAGCTCAGGCAATCTCCAAGGCAGTAGCCCTATCAAAATGAAAGTC 2 	240

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Sequence 139, Application US/09984827

Sequence 139, Application US/09984827

Publication No. US2003005623441

SEREMAL INFORMATION:
APPLICANT: DENEFILE, PATRICE
APPLICANT: RANOULD-REGUIGNE, ISABELLE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: CAMHIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USFRENCE:
TITLE OF INVENTION: DETECTION METHOUS AND KITS THEREFOR
TITLE OF INVENTION: DETECTION METHOUS AND KITS THEREFOR
FILE REPRENCE: 103006.0522-00000
CURRENT FILING DATE: 2002-001
PRIOR FILING DATE: 2000-10-11
PRIOR FILING DATE: 2000-10-31
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SOFTWARE: PALENTING DATE: 2000-10-31
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; ORGANISM: Homo sapiens
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PRIOR APPLICATION NUMBER: FR 00/14037 PRIOR FILING DATE: 2000-10-31 NUMBER OF SEQ 1D NOS: 161 SOFWARE: Patentin Ver. 2.1 SEQ 1D NO 140
                                                                                                                            Matches 2892; Conservative
                                                                         ORGANISM: Home sapiens
                                                                                                                   Similarity
                                                                                    US-09-984-827-140
                                                                 TYPE: DNA
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APPLICANT: ARNOULD REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
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Publication No. US20030056234A1
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                                                       ROSIER-MONTUS, MARIE-FRANCOISE ARNOULD-REGUIGNE, ISABELLE
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APPLICANT: DENEFIE, PATRICE
APPLICANT: ROSIRF-MONUS, MARIE-FRAI
APPLICANT: ARNOULD-REGUIGNE, ISABELI
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APPLICANT: DUVERGER, NICOLAS APPLICANT: CAMBIEN, FRANCOIS TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL SENE, IHEIR USES, AND TITLE OF INVENTION: DEFECTION METHODS AND KITS THEREFUR FILE REFERENCE: 03806.0522-00000 CURRENT PAPLICATION NUMBER: US/09/984,827 CURRENT FILING DATE: 2002-04-01 PRIOR PAPLICATION NUMBER: 60/254,108 PRIOR PLING DATE: 2000-12-11 PRIOR APPLICATION NUMBER: FR 00/14037 PRIOR APPLICATION NUMBER: FR 00/14037 PRIOR APPLICATION NUMBER: 10/14037 PRIOR APPLICATION NUMBER: 10/14037 PRIOR APPLICATION NUMBER: 10/14037	s S·	Query Match  Best Local Similarity 100.0%; Pred. No. 5;  Matches 2892; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  A ACAGGGATGGTGCTGTAATCTCAGTTACTCGGGAGGTGAATGA 66  Oy A ACAGGGATGGTGCTGTAATCTCAGTTACTCGGGAGGTGAATGA 66	ACAGAGATGGCACCATTGCACCTGTANTCTCACTAACTGCACAGTTGCAATGTGCACCTTGCACTTGCACCTGGCACCAAAAGTGCACCATCTCAATTTGCATTTGCACCAAAAAAAA	Db 121 AAAAAAAAGAATGATTTTGGTGGTCGACTTCAAATAGGTAGG	11	Db 361 AAAATGAAGAAGAGGGGGAAATGACTGATTGCCAGGAATTTGCGAAG 420  QY 421 CTGAGGCCAGAGGCCGGGCAATGACTGCTAATGCCAGGATTTGCGAAA 480  UTLITITITITITITITITITITITITITITITITITITI	541 CCCAGCTACTIGGAGGCTAAGTGGGAGGATCGTTGAGCCCAGGGAGTCACA 60 111111111111111111111111111111111111	661 AAAAAAGAAATGAAAGAAAGAAAGAAGGAGGAGGAGGAGAGAGAGGAG

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CURRENT EDETICANT: DENEFLE. PATRICE
APPLICANT: DENEFLE. PATRICE
APPLICANT: ROSIER-WONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: CAMBIER, FRANCOIS
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806-0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT APPLICATION NUMBER: US/09/984,827
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEO ID NOS: 161
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Sequence 142, Application US/09984827 Publication No. US20030056234A1 GENERAL INFORMATION:
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2821 GCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAACCTATAAANGAACTAGTCC 2880 11111111111111111111111111111111111	RESULT 10 105-09 984-827-143 Sequence 143. Application US/09984827 Sublication No. US20030056234A1 GENERAL INFORMATION: APPLICANT: BENEFIE, PATRICE APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE APPLICANT: APPLICANT: AUGUS AUGUS AUGUS APPLICANT: AUGUS	TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABOAL GENE, THEIR GSES, AND TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABOAL GENE, THEIR GSES, AND TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFORE 103806.0522-00000 CURRENT APPLICATION NUMBER: US/09/984,827 CURRENT FILING DATE: 2002-04-01 PRIOR APPLICATION NUMBER: 60/254,108 PRIOR PRIOR APPLICATION NUMBER: FR 00/14037 PRIOR APPLICATION NUMBER: FR 00/14037 PRIOR SEQ. ID NOS: 161 SEQ. 100 NOS: 161 NOS:	mo sapiens 3	ative 0: Mismatches 1: Indels 0: Gap CAGGTGCTGTAATGTCAGTTACTCGGAGGTGGAGGTTGCAGTTACTCGGAGGTGGAGGTTGCAGTTGCAGTTACTCGGAGGTGGAGGTGGAGTGAGT	GUULLAGAT COUNCETT TGUAG UN GOGGA AANAAG BIDAAAN AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	TTANTAACACTCTGCTTTATAACATCATTCTGCCAAGGACTCAAAGGATTCAACA HITHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH

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APPLICANT: WOSIER ANDIUS, MARIE-FRANCOISE

APPLICANT: AROULD-REGULD. ISABELLE

APPLICANT: AROULD-REGULD. ISABELLE

APPLICANT: CAMBIEN, FRANCOIS

TITLE OF INVENTION: POLYWORPHIC SEQUENCES OF THE HUMAN ABJAI GENE, THEIR USES,

TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFYSK

FILE REFERENCE: 03806.0522-00000

CURRENT APPLICATION NUMBER: 05/09/984.827

CURRENT APPLICATION NUMBER: 60/254,108

PRIOR ETLING DATE: 2000-10-31

NUMBER OF SEQ 1D NOS: 161

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APPLICANT: BENEFIE; PATRICE
APPLICANT: ROSIEK-MONUUS, MARIE-FRANCOISE
APPLICANT: ROSIEK-MONUUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES,
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806,0522-00000
CURRENT APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
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                                                                             2463 AAAGGAAAAAAAAATGCGGAAAGCAGATTTAGAGGAAGAAATCCACTGGTGCCCTT
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Publication No. US20030056234A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2
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Qy 1021 TCGACTCACTGTAACCICTGCCTCCCGGC	US-09-984-827-148
Db 961 TTATTITCTTGACACGGAGTCTIGCTCT	ORGANISM:
Oy 961 TIATTTTTCTTGACACGGAGTCTTGCTC	; 550 11 NO 14a ; ENGRA 2893
Db 901 CCTGGCCTTGGGCTTTAGAAAGCTCAT	SOFTWARE: Patentin Ver. 2.1
Qy 901 CCTGGGCCTTGGGCTTTAGAAAGCTCATC	PRIOR PETERS 2000-10-31 PRIOR FILLING DATE: 2000-10-31 NUMBER VIE SED TO NOS. 161
Db 841 CCCCAAAACCCAATTATTGACCAAGGT	PRICK FILLING DATE: 2000-12-11 . DRICK FILLING DATE: 2000-12-11
Qy 843 CCCCAAAACCCAATTATTGACCAAGGT	CURKENT FILING DATE: 2002-04-01
Db 781 GATGAAACAGAGCAGAAAGACTTTACG	; IIII. OF INVENTION: DETECTION METHOUS AND KITS THEREFOR: FILE REFERENCE: 0306, 0522-00000 . : CHREWIT ADDITON NIMBER TICOGGARA M.77
UY 781 GATGAAACAGAGGGAAGACTITAGG	FITTE OF INVENTION: POLYMORPHIC SEQUENCES OF
Db 721 GAGGGGGGGGAGGAAGGAAGGAAGGAAGGAAGGAAGGA	APPLICATE: DUVERGER, NICOLAS APPLICATE: DUVERGER, NICOLAS
Qy 721 GAGGGGGGGGGAGGAAGGAAGGAAGGA	
Db 661 AAAAAAGAAATGAAAGAQAAAGAAAGA	U
Oy 661 AAAAAAAAATGAAAGAAAGA	US 09.944-827-148 : Sequence 148, Application US/0984827
DD 601 CTGAGCCATGATTGGATCACTGCACCCC	RESULT 14
Oy 601 CIGAGCCAIGATIGGATCACIGCACICC	Db 2881 CGCAAAAACCCC 2893
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Oy 481 ACCCTGTCTGTAGAAAAAAAAAAAAAAAAAAAAAAAAAA	25.21 GOTTTGACCGATAGRAACGTCGGGGGGCGCGAACGAALGTATAAAAGGAAACTAGTCG
	QY 2761 TGAGTGAACTACATAAACAGGCCGGGAAAGGGGGCGGGAGGAGGAGGAGGAGGA
Db 361 AAGATGAAGAACAGGCCGGGCACAATG	
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Qy 241 TTFAATAACACTCTCTGCTTTATAACAT	2321 GGC1GCCGGGGAACG1GGACTAGAGAGTC1GCGGCGCGCAGCCCCAGGCCCAGGCCT1CCGGCGCGCGCGCGGCGGAGGCGGAGGCGAGGC
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Ov 121 AAAAAAAAAAAGAATGATTTTGGTGGTCG	Db 2401 GGGAGATTCAGCCTAGAGCTCTCTCTCCCCCAALCCTTCCGTCGGGTGAGGAAACTAAC 2450
OY 01 GECENATIONED 111111111111111111111111111111111111	OY 2401 GGGAGATTCAGCCTAGAGCTCTCTCCCCAATCCCTCCGGCGGGGGGAAACTAAC 2460
<b>-</b> ;	OY 2141 CACCCCAGCCTAGGCCTTTGAAGGAAACAAAGGCAAAATGATGGCGTCCTGA 2400 [[[[[[[[]]]]]]]]] [bb 214] CACCCCAGCCTAGGCCTTGAAGGAACAAAGACAAAAGAAAAATGATGGCGTCTGA 2400
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89.5%; nilarity 100.0%;	UY 2281 CAUSTIFGTGGGGGGAAAACAAAAGCACCCATTACCCAGAGGACTGTCCCCCT 2340

ö 1021 TEGACTERACTERARCHERGETCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCTGA 1080 AGAGTTTGAGACCAGCTGGATAACATGGCAAA 480 540 AGGATCCCTTGAGCCCAGGGGTCAGTCTACA 600 999 840 120 180 180 240 240 ATCATICIGCAAGGAGTCAAAGGTTTCAACA 300 360 540 999 AAAGAGGAGAGAGAGATGAGGGGAGGAGG 720 FTATTCTTTGACTGAGGCGAAGGGGGTCCGCTCT 900 120 ICTCTGGCCTTTCTGAGATCCATCCCTTTCTTT 960 Gaps reteagtiactegggaggtggaggtgcaatga 60 CAGCCTGGGTAGACAGAGCAAGACCCTGTCTCA GTAAATTGCTCATCATGTGGTTGTCAAGTTTGA BACTTCAAATAGGTAGGAGAGGAGAGG TCTCTAAAATCATGCTAGGAAAGATAACACCT SGAAGACAGAATATACATCTTCTCTCCATTTTA TCTCTAAAATCATGCTAGGAAAGATAACACCT DB 9; Length 2893; ; 0 Indels 1; re 2891.4; ed. No. 0; 4ismatches õ

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PRICK FILING DATE: 2500 12 11
PRICK APPLICATION NUMBER: EK GG/34037
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: Publication No. US20030056214A1
; GENERAL INFORMATION:
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Pred. No. U;
                                                                                       Hest Local Similarity 100.0%; Pred. No. U. Matches 2892; Conservative 0; Mismatches
PRICK FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 149
                                                      : ORGANISM: Homo sapiens
JS-C9-984-827-149
                                     LENGTH: 2893
                                             TYPE: DNA ORGANISM: 1
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Best Local
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Ογ	1561	GUSCAGCIUTETCATGCACCTCATTCTGGCAAAACTCAGGTCAAACTGTGAAGAGTCT 1620
qa .	1561	NGCTC1CICATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCT 162
ς	1621	AAATGTGAALCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGACCTT 1680
qa	1621	TGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGGCCTT 168
Oy	1681	GIGGCCICCACGIGCACTTCCAGGGCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGT 1740
qu	1681	30cc1ccacg16cact1cca666cc16c11666cc1ct1ctac6661ct6fcc16ag1 174
Oy	1741	TICAGGGCAGAITCATATTAGACTCTTCACAGTTTGACCTGAGTTT 18
qa	1741	TTCTATGAATCCTTCAGGGCAGATTCATATTAGACTCTTCACAGTTTGACCTGAGTTT 1
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đ	1801	GCCAGATAAGGIGACATTAGTITGTIGGCTIGATGGATGACTIAAATATTAGACA 186
Οy	1861	16GT61GTAGGCCTGCATTCCTACTCTTGCCCTTTTTTTGCCCCTCCAGTGTTTTGGGT 1920
qa	1861	GTGTGTAGGCCTGCATTCCTACTCTTGCCTTTTTTTTGCCCCTCCAGTGTTTTGGGT 1922
Qy	1921	AGTITIGCTCCCCTACAGCCAAAGGCAAACAGAGAAGTTGGAGGTCTGGAGTGGCTACAT 1980
qu	1921	ITTIGCTCCCCTACAGGCAAAGGCAAACAGAGAAGTTGGAGGTCTGGAGTGGCTACAT 198
6	1981	AAITTTACACGACIGCAAIICTCTGGGTGCACTTCACAAATGTATACAAACTAAATACAA 2040

040	166 100	160 160	22C 220	280 280	340	400 400	450 466	520 520	580 580	640 640	007	75U 75U	820 820	680 880	
	GTCCTGTGTTTTATCACAGGAGGCTGATCAATATAATGAAATIAAAAGGGGCTGGTG 2 	CATATIOTICIGAGITITICETICITICATITICATICATICATICATIVATA STATEMENT (GGCC 2   11   11   11   11   11   11   11	TCCTTCCTCTCAATTTATGAAGAAGCAGTAAGATGTTGGTCTGGGGTCGTCTGAGGGA 2   1   1   1   1   1   1   1   1   1	CCTUGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATGAAAATCAAAAGT 2 	CAGCTFIGEGGGGAAAACAAAAGCCCATFACCAAGAGGACTGTCCGCGTCTCCCCT 2	CACCCAGCCTAGGCCTTGAAAGGAACAAAGACAAGAAAAATGATTGGGGTCTGA 2. 	GOGAGATICAGOCTAGAGGTGTCTCTCCCCCAATCCTGCCTCCGGGTGAGGAAACTAAG 2   1   1   1   1   1   1   1   1   1	AAAGGAAAAAAAATTGCGGAAAGCAGGTTTAGAGGAAACAAATTCCAGTGTGTGCGCTT 2: LLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	GGCTGCGGGAACGTGGACTAGAGAGTCTGCGGTGGCGGGGGGGG	GCGTCFTAGGCCGGCGGGCCGGGCGAACGCGAGGCGCAGACGCGCACGCTAAGACA 2 HILLHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	CONGUESTA COCTOCA COCOCO COCOCO COCO COCOCO A COCOCO A COCOCOCO	TROTGGGCGCTGAACGTCGCCGTTTAARGGGGGGGCCGGGCTCGAGGTGCTTTCTGC 2 FILLITHTHTHTHTHTTTTTTTTTTTTTTTTTTTTTTTTT	TGAGTGACTGAACTACATAAACAGAGG 		CGGCAAAAACCC 2893 11111111111 CGGCAAAAACCC 2893
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/cgn2_6/ptodata/l/ina/5B_COMB.seq:*
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GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd
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length: 2000000000
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Maximum DB seq
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APPLICANT: Statewicz, Brian S., Oldroyd, Giles Edward, APPLICANT: Statewicz, Brian S., Oldroyd, Giles Edward, APPLICANT: Salmeron, John M., Roumens, Catus TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PLANT TITLE OF INVENTION: PATHOGEN RESISTANCE CORRESPONDENCE ADDRESS: 15 CORRESPONDENCE ADDRESS: ADDRESSE: Whinston STREET: One World Trade Center STREET: One World Trade Center STREET: Saite 1600 CITY: Portland STATE: Oregon CITY: Ortland STATE: Ortland STATE: Ortland STATE: Ortland STATE: Onlined States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 5151-45038
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/680,327 FILING DATE: July 11, 1996 CLASSIFICATION NUMBER: 08/310,912 FILING DATE: September 22, 1994 CLASSIFICATION NUMBER: 08/310,912 FILING DATE: September 22, 1994 CLASSIFICATION NUMBER: 08/227,360 FILING DATE: APRIL 13, 1994 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: DOW, Alan. E. REGISTRATION NUMBER: 35,123 PERFORMATION NUMBER: 35,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     us/08/680,327
US-08-680-327-2
; Sequence 2, Application US/08680327
; Patent No. 5859321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double stranded TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10968 base pairs
TYPE: nucleic acid
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                                                                                   GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Staskawicz, B. S. et al.
TITLE OF INVENTION: PRE Protein and Nucleic Acid Seq.conves: Composition of Intle OF INVENTION: And Methods for Plant Pathogen Presistance: ITLE REFERENCE: 51700
CURRENT APPLICATION NUMBER: US/09/228,246
CURRENT APPLICATION NUMBER: 08/680,327
EARLIER APPLICATION NUMBER: 08/680,327
EARLIER APPLICATION NUMBER: 08/310,912
EARLIER FILING DATE: 1994-09-22
EARLIER FILING DATE: 1994-04-13
NUMBER: OF SEQ ID NOS: 5
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                                                                                                                                                                               Db 10868 GASCTICAIGAACCAAAGIIACCIIITTTTIIITTAATGGCAITACTTIG :9518
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                                                                                                                                                           269 GTTTTTCACCAGCGGGGGTTCTCTCTTTTTTTTTTGTGGTTTTCAGTTG 419
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Pred. No. 7.8;
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTALL.
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                                         503
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                                       0; Mismatches
                                                                                                                                                                                                                                                                                             : Sequence 1, Application US/09228246
: Patent No. 6245510
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Patent No. 5789544
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APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MIYAMURA, TATSUO
Query Match
Best Local Similarity 55.0%;
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Matchis 61, Conservative
                                       61; Conservative
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US-09-228-246-1
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237 CTACCCTCGGGTTGGTGGCGTTGGGGATAGGTTGTCGCCTTCCACGAGGTTGCGGCCCC 178
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                       Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                   FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,303
FILING DATE: 12.MAY-1995
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUN-1993
APPLICATION NUMBER: JP 152487/1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Oblon, No. 5789544man F.
REGISTRATION NUMBER: 24,618
REFENCE/DOCKET NUMBER: 4169-003-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                  CURENT APPLICATION DATA:
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,195
FILING DATE: 05-JUN-1995
C'ASSTFICATION: 514
                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC computible
OPERATING SYSTEM: PC-DUS/MS-LOS
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IMMEDIATE SOURCE:
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TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
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LENGTH: 1037 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: doub
ADDRESSEE: P.C.
STREET: 1755 S. J
CITY: Arlington
STATE: Virginia
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Matches 101, Conserv
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                                                                                          U.S.A.
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OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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APPLICANT: SAITO, IZUMU
APPLICANT: MATSUURA,
APPLICANT: MATSUURA,
APPLICANT: BONDA, YOSHIHARU
APPLICANT: SEXI, MAKOFO
APPLICANT: SAITO, TOTAL
APPL
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MFDIUM TYPE: Floppy disk
COMPUTER: IHW PC compatible
OPERATING SYSIEM: PL-TOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 24,638
REFERENCEZOUKET NUMBER: 4169-003-0
TELEPOMMUNICALD NINECRMATION:
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APPLICATION NUMBER: JP 152487/1992
FILING DATE: 1-JUN-1993
ATTORNEY/AGENI INFORMATION:
NAME: Opton, NO. 6069944400 F
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APPLICATION NUMBER: US/08/446,303
FILLING DATE:
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: Patent No. 6063904
: GENERAL INFORMATION:
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ANTI-SENSE: No
ORIGINAL SOUGE:
ORGANISM: Hepatilis C virus
:MMEDIATE SOUCE:
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TELEX: 24885 PAT UR
INFORMATION FOR 859 15 NO: 3
SEQUENCE CHARACTER STICS:
LENGTH: 1037 base pairs
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COUNTRY: U.S.A.
ZIP: 22202
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STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington
SIATE: Virginia
COUNTRY: U.S.A.
                                                                      APPLICANT: SAITO, IZUMU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HENDA, YOSHIKAZU
APPLICANT: HENDA, YOSHIKAZU
TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROLEIN OF THILE OF INVENTION: METHOD FOR PRODUCING ECTOPROLEIN OF WINNER OF SUCCERCES: 9
CURRESPONDENCE ADDRESS:
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ZIP: 42202

COMPUTER READABLE FORM:
MENTOW TYPE: Floopy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-UOS/MS:DAS
SOPTWARE: PATCHIO Release #1.0. Version #1.25
CUKRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/446,303
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MCLEGULE TYPE: DNA (genomic)
               MIYAMURA, TATSUO
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CLASSIPICATION: 435
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0 EUP PERMENEN FORDET CONTENTEN TO BETTEN TO SOCIO CONTENCE A GOOD TO CONTENTE A GOOD TO CO k.f%, Score 80.8; DB 3; Length 10\*7; 45.f%; Pref. No. 2.6; 4f.fvc 0; Mismatches 117; Indels 0; Chaserdative 1111

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APPLICANT: Hendrickson, Eric

APPLICANT: Hendrickson, Eric

TITLE OF INVENTION: A No. 6171857el Loucine Zipper, KARP-: and

TITLE OF INVENTION: Methods of Regulating DNA Dependant PLYCH Kindse Activity

TITLE OF INVENTION: Methods of Regulating DNA Dependant PLYCH KINGSE ACTIVITY

CURRENT APPLICATION NUMBER: US/09/173,914

CURRENT FILING DATE: 1998-10-16

FARLIER APPLICATION NUMBER: 60/064.557

EARLIER APPLICATION NUMBER: 60/064.557

SOFTHARE: FALING DATE: 1997-10-17

NUMBER OF SCO 1D NOS: 35

SOFTWARE: FASLSEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION: Anderson et al. APPLICANT: Kevin P. Anderson et al. TITLE OF INVENTION: Compositions And Methods For Pretagent of Hepatitis C V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1629 AGAGGAATCTCACATTTGGCTTTCACCTCAGTGGGGGATCCAGAATTTCAAAA;GTGC 1570
                                                                       177 TOGGAAGTCTTCCTAGTCGCGCGCACCCAGCGGCCCCTGGGAGGCAACAGTAG TB
                                                                                                                                     227 GGAAGAACCICACTIICAGAAGAAGAACAACAATAAGCIIGGGTTIIITAGIAGTGGGAAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 AGACAAACAGIAAGCIIGGGTITIIGAGCAGGGGGGGGTTCICTCATI;I;ICTIGIGG 309
                                                                                                                                                                  e: Gaps
237 CIACCCTCGGGTTGGCGAGCCTTGGGGATAGGTTGTCGCCTTCCA GAGGTTGGGGGG
                                             167 ACCCTGGGCGTGCTGGCTGAGGGAACAIGGCATGTTGGCCTCACCTGAACTTGCTGTTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30.4; DB 4; Length 2473;
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STGRAGE
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2: Law Offices of Jane Massey Licata
66 East Main Street
                                                                                                                                                                                                                              287 GITCICTCATITITICTIGIGGTTTIGAGTTGGGGAT 324
                                                                                                                                                                                                                                                     57 LTACGITTGATTTTCTTTGGGGTTTTGGATTTGGGT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *10 TTTTGAGTTGGGGATTGGAGGGAGGGAGGGAAG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 5.6;
0; Mismatches
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SOFTWARE: WORDDERFECT 6.1 FOR WINDOWS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/988,321B
FILING LAFF: December 10, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 37, Application US/08988321B Patent No. 6174868
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09173914
Patent No. 6171857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ::RGANISM: Mesocricetus Auratus
US (%-173-914-3
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Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offic
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US-09-174-914-3/C
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111 CCACGGGCGTCCCTGCTGTCACCTCTGGCGCTGCCTTCCAGGGCTCCCGAGGCCACACGC 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 GAACCTCACTTTCAGAAGAAGAACAAAACAGTAGGTTTTTCAGCAGCGGGGGTTC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 CACCAACGATCTGACCACCGCGGGAACTTGACCTCCTGTGGGCGGCGGTTGGTGTAC 379
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US-08-397-2208-25/C

) Sequence 25, Application US/08397220B

) Patent No. 6284458

) GENERAL INFORMATION:

) GENERAL INFORMATION:

) TITLE OF INVENTION: Compositions And Methods For Treatment

) TITLE OF INVENTION: OIL Hepatitis C Virus-Associated Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 8.4%; Score 30; DB 4; Length 686; Best Local Similarity 46.3%; Pred. No. 3.9; Matches 99; Conservative 0; Mismatches 115; Indels
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OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Jane Massey Licata, Esq.
STREET: 210 Lake Drive East, Suite 201
CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 ICTCATITITICITIGACITITICAGITICGGGAT 324
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                                                                                                                                                                                                                                                                                                                                                                              ISPH-0245
                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/945,289 FILING DATE: September 10, 1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DAIE: 09-Mar-1995
                            08/650,093
                                                                                                                                                                             08/397,220
                                                                                                    08/452,841
                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBÉR: 32,257
REFERENCE/DOCKET NUMBER: ISI
TELECOMMUNICATION INFORMATION:
                                                                                                                         FILING DATE: May 30, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U8/397,
FILING DATE: March 9, 1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/650
FILING DATE: May 17, 1946
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/452
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (856) 810-1515
TELEFAX: (856) 810-1454
INFORMATION FOR SEQ 1D NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,2
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COUNTRY: USA
21P: 08002
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: Single
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TI-SENSE: NO
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US-08-988-321B-37
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FILING DATE: May 30, 1995
APPLICATION NUMBER: 08/397,220
FILING DATE: March 9, 1995
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992
ATTORNEY/AGEN INFORMATION:
NAME: Jane MASSEY Licata
REGISTRATION NUMBER: 32,257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1SPH-
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8.4%; Score 30;
Best Local Similarity 46.3%; Pred. No.

Matches 99; Conservative 0; Mismatci
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COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAR: (609) 779-8488
INFORMATION FOR SEQ 10 NO: 25:
SEQUENCE CHARACTERISTICS:
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08866590
Patent No. 5939321
GENERAL INFORMATION:
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REGISTRATION NUMBER: 37094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 686
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STREET: 1 C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 30; DB 4; Lengtl, 685;
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MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STGRAJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 46.3%; Pred. No. 3.9;
Matches 99; Conservative 0; Mismatches 115; 15dels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/650.093C
FILING DATE: 17-May-1996
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA: 08/452,841
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                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Jane MASSEY Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0633
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                                                                                   APPLICATION NUMBER: PCI/JP93/01293
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STREET: 66 E. Main Street
CITY: Marlton
                                                                                                             FILING DATE: 10-Sep-93
APPLICATION NUMBER: JP 5-87195
FILING DATE: 14-Apr-93
APPLICATION NUMBER: 07/945,289
FILING DATE: 10-Sep-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 25
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OPERATING SYSTEM: Windows 95
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patent No. 6391542
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
INFORMATION FOR SEQ ID NO: 25:
           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: Single
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                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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COUNTRY: USA
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111 CCACGGGG FCGFFGFGFGFGAGTFTGGCGCTGCCTFCCAGGGCTCCCGAGGCACACGC 170
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                                                      Gaps
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DB 4; Length 686; 3.9;
                                                   0; Mismatches 115; Indels
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APPLICANT: Takahara, Kazuhiko
APPLICANT: Takahara, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
CORRESPONDENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866,550
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double

STRANDEDNESS:

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Rest Local Similarity 52.4%; Pred. No. 11;
Matches 66; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                          CITHER INFORMATION: /product= "murise mTII protein." US-08-866-650-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Greenspan, Daniel S
APPLICANT: Takahara, Kazuhiko
APPLICANT: Takahara, Guy G
APPLICANT: Hoffman, Guy G
NITISE OF INVENTION: Mammalian Colloid-Like Prote...
CHRESIONEDENCE ADDRESS:
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APPLICATION NUMBER: US/09/021,287
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ALCANEY CAGENT INFORMATION:
NAME: Belson, Bennett J
REGISTRATION NUMBER: 37094
REFERENCE/DOCKET NUMBER: 960296,93839
TELESOMMONICATION INFORMATION:
:ELEPRONE: 608-251-9166
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COMEUTER: SM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DGS
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STREET: 1 South Pinckney Street
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APPLICATION NUMBER: 08/866,650
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Patent No. 5981717
GENERAL INFORMATION:
TELECTMMUNICATION INFORMATION:
TELEPHENE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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                                                                               SEQUENCE CHARACTERISTICS:
LENGIH: 4771 base pairs
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                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
TOP/LOGY: linear
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LOCATION: 611..3652
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261 GCTGAG 266
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ZTP: 53703
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Cliff: Ma
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US 09-021-287-2
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102 AATGACCAGAGAGGGGGTCCCTGCTGTCAGCTCTGGCCGCTGCCTTCCAGGGCTGCGGA 161
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                                                                                                                                                                         Ouery Match 8.4%; Score 30; DB 2; Length 4771; Best Local Similarity 52.4%; Pred. No. 11; Matches 66; Conservative 6; Mismatches 60; Indels
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                                                             ; COCATION: 611..3652
; OTHER INFORMATION: /product- "murine mTll protein"
US 09-021-287-2
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: OTHER HWERMALDEN: Zeroduct - "aurine mill protein"
US-09 246 473-2
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APPLICANT: Takahara, Kazuhiko
APPLICANT: Hollman, Guy G
TITLE OF INVENTION: Mammalian Tolloid-Like Protein
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REACHER FORM:
MEDIUM TYPE: FORSPY OF SK
COMPUTER: THM PY COMPATION COMPUTER: THM PY COMPATION COMPUTER: THE OF COMPATION SYNS-TH'S
SOFTWARE: PARTITUDE OF CASC #1.0, Version #1.30
CURRAT APPLICATION DAIA
APPLICATION NIMBER: 35/59/240.473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ANDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Plackney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09240473
Patent No. 6297011
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berson, Bennett J
REGISTRATION N.MBER: 47094
REFERENCE/PROKET NUMBER: 950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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AITORNEY/AGENT INFORMATION:
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LENGTH: 4771 base pair:
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STRANDEDNESS: double
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CITY: Madison
STATE: WI
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US-09-240-473-2
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195 GGCATGTTGGCCTCAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGAAGACA 254
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                                                                                                                                                                                                                                                                        APPLICANT: El:Deiry, Wafik
APPLICANT: El:Deiry, Wafik
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Banner & Allegretti, LTD
STREET: 1001 G Street. NW suite 1100
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01107.49698
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COMPUTER READAHLE FORM:
MEDIUM TYPE: FLOEPY disk
CMEDTER: IHM PC compatible
OPERATING SYSTEM: PC-KNS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/574,043
                                                                                                               4300 GCCACAAATCTGGCTTTTTTA 4279
                                                                                                                                                                                                                       Sequence 7, Application US/08795015
Patent No. 5871968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           =
                                                                                          255 AACAGIAAGCITGGGTTTTCA 276
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REGISTRATION NUMBER: $2,141
REFERENCE/DXCKET NUMBER: $1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHROMOSOME/SEGMENT: 6p21.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ 15 NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENI INFORMATION:
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202,568,9299
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LENGIH: 5143 base pairs
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Bost Local Similarity 50.7%
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
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US-08-795 015 7/c
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                                                                                                                                 162 GCCACACGCTGGGCGTGCTGGCTGAGGGAACATGGCATGTTGGCCTGAGCTGAGGTTGCT 241
                                                    102 ANTSANCAGGGGAGGGGGGGCCTGCTGTGAGCTGTGGCCTTGTAGGGGTGTGGGA 161
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Best Local Similarity 50.7%; Pred. No. 11:
Matches 72; Conservative 0; Mismatches 70: 10: 10:018
                   60; Indels
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APPLICANT: El-Derry, Wafik
APPLICANT: Vogelstein, Bert
ITILE OF INVENTION: p21WAF1 Derivalives and Diagnostic
ITILE OF INVENTION: methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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CURKENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,043A
Pred. No. 11:
0: Mismatches
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CLASSIFICATION: 514
ATTORNEY-AGENT INFORMATION:
NAME: Kadgan, Sarah A.
REGISTRATION NUMBER: 32,141
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Street, NW suite iloo
CTTY: Washington
STATE: DC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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: Sequence 7, Application US/08574043A
: Patent No. 5807692
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.508.9190
TELEFAX: 202.508.9299
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POSITION IN GENOME:
CHROMOSOME/SEGMENT: 6p21.2
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Best Local Similarity 52.43
Matches 66; Conservative
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EDNESS: double
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261 GCTGAG 266
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Sequence: Application US/0875i189
Fatent No. 5919656
GENERAL INFORMATION:
APPLICANT: Harfington, Lea A.
APPLICANT: Mobinson, Murray O.
TITLE OF INVENTION: 12
CURRESPONDENCE: 12
COMPRESPONDENCE ADDRESS:
ADDRESSE: Amagen, Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUMPRY: USA
CITY: 1840.
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Best Local Similarity 48.8%; Pred. No. 14;
Matches 81; Conservative 0; Mismatches 85; Hebits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CUMPUTER FRANCHIEF FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPOTER: Floppy disk
COMPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/751.189
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY ACENT INDORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: A-433
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7881 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: May 9, 2003, 16:36:08
Job time : 31.3027 secs
                                              255 AACAGTAAGCTTGGGTTTTTCA 276
1 1 11 11 1 11111 1
4300 GCGACAAATCTGGCTTTTTTTA 4279
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; Sequence : Ap
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May 9, 2003, 12:47:56 ; Search time 599.179 Seronds (without alignments) 9649.520 Million cell updates/sec
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GenCore Version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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| 2. em_estba:"
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| 10. qb_est2:"
| 11. qb_est2:"
| 12. qb_est3:"
| 13. qb_est5:"
| 13. qb_est5:"
| 14. qb_est5:"
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| 7. qb_qss:"
| 8. em_qss_htm:"
| 8. em_qss_htm:"
| 9. em_qss_htm:"
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Maximum DB seq length: 2000000000
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357
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_mus:\* em\_gss\_other:\* em\_gss\_pro:\* em\_gss\_rod:\*

			description		AL598654 DKFZp586N	AU135588	535577254 PB657864	244377 HSC12BC81 n	BG184217 303216 MA	Ally2+82 Petracdon
SUMMARIES			QΙ		AL698654	AU135588	BB657864	2.44377	12 BG384217	CNS02D01
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			ore Match Length DB ID		547	736	619	292	535	885
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υ		35.4	5	937	~	CNS006ST	AL065880 Drosophil
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ز		35.2	, 2,	1201	1 1	CNS0162E	AL106208 Drosophil
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	4.5	34.6	9.7	884	- 1	CNS006U0	AL065923 Drosoph11
						ALIGNMENTS	
RES	11.1						
A1.6	98654						
LOCUS	LOCUS DEFINITION		AL598654 DKF2p686N12	10%_r1	686	547 bp mRNA linear (synonym: hlcc3) Homo sapiens	linear EST 21-MAR-2002 omo sapiens CDNA clone
J)W	NO1553.	DKF.	2p686N1. 38654	209 57	, mknA	NA sequence.	
VER	SION	A1.6	98654.1	61:19	96191	.94	
KEY	KEYWORDS	EST					
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			Eukaryota;	, Metazo	120a;	Chordata; Craniata;	ш
REF	ERENCE	Mam,	malla; t (bases i	Euthern to 54		: Catarrnin	; Hominidae; Homo.
•	AUTHORS	Due	Duesterhoef	tt.A.,	Laube	er, J., Mewes, H.W.,	Gassenhuber, J. and Wiemann
F	T111.E	.s. EST	(Dueste	rhoeft		( )	
ירי	JOURNAL	Onpu	Unpublished (1999)	1 (1999		i	
000	COMMENT	Conte	tact: Du	iesterh	erhoeft	Α	
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		con	sortium	of the	Ger Ger	milden/Germany) with	nin the CDNA sequencing
		Sol	sl seque s clone	<pre>l sequence available. clone (DKFZp686N12109)</pre>	aile 686b	uble. 112109) is available	erlin
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VERSION
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Mammalia, Eutheria, Primates, Catarrhicz, Romin, Jaer Homo.
1. (bases 1 to 736)
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HRI human cDNA project; 5' - 5 3' -end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                157 COCCAGCCACCCACGCTGGCGTGCTGGCTGACGAACATGGCATGTTGGACTCAGCTGAGG 216
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Yamamoto.J., Wakamatsc.A., Nakamera,Y., Nadai.T., Sidano.S. an
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                                                                                                                     /clone="DKEZp686N12109"
/clone_ib.*686 (synonym: hice:y"
/tissue_type="human skeletal muscie"
/dev_stage="adult"
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
1781: 81-438-52-3975
Fax: 81-438-52-3986
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81.8%; Pred. No. 1.4e 33;
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/note="Vector: pME18SFL3"
199 c 199 g 170
                                                                  /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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/db_xret-"taxon:9606"
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Location/Qualifiers
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Unpublished (2000)
Centact: Takao Isogai
Genomics Laboratory
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Mis muscrilus
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.
1 (bases: 1 to 619)
Arakawa.T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horli,F., Ishli,Y., Ito,M., Rawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Sakai,C., Sakai,K., Sano,H., Sasaki, D., Shibata,K., Shinayawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Tagamani,M., Tagawa,A., Takakaya,F., Takeda,Y., Tanaka,T., Toya,T.,
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
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URL:http://genome.gsc.riken.go.jp,
Carninci.P./Senome.gsc.riken.go.jp/
Carninci.P./Shibata.Y. Hayatsu.N., Sugahara,Y., Shibata.K., Itoh
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Normalization and subtraction of cap-trapper-selected cDNas to
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wagi.K., Eujiwake.S., Innue.K., Togawa.Y., Izawa.M., Ohara,E.,
Hatahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
.S., Kawaii,J., Okazaki,Y., Muramatsu,M., Innue,Y., Kira,A. and
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Science: Contact (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7.22 Suchiro-orb, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Pax: 81-45-503-9216
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BB657864 REKEN Full-length enriched, 12 days embryo eyeball Mus
musculus cDNA clone D230019D04 5', mRNA sequence.
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Length 736;
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0; Mismatches 43
           Score 144.2;
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80.4%;
Query Match
Best Local Similarity 80.4
Matches 181; Conservative
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contributed to prepare mouse tissies. Ist strand cDNA was primed with a primer [5' GAGAGAGAGAGAGACACTGAGTHITTITTITTIVN 3'], cDNA was
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Auffray.C., Behar,G., Bois,F., Bouchier,C., do Silva,C., Beetisnes
Am.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lacy,B., Corenzo,F.,
Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
                                         Computational Analysis of Full-Length Mouse cashs compared with Human Genome Sequences, Mamm. Genome. 12, 67:-677 (2031) Please visit our web site (http://genome.ass.riken.go.jp) for larther details.
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Pred. No. 1.9e-10;
0; Mismatches 27; Indels 11:
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the .minscore 18
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Pathenkruny.S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
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                                                                                                                  Genexpress_library_idt: C; Genexpress_sequence_idt: ylc-12b08
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Location/Qualifiers
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1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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Eukaryota; Metazoa; Thordata; Craniata; Vertebrata;
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 14;
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Pred. No. 6.8e-10;
0; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases ca
                                                                                 Email: genexpress!genethon.fr
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                                                                                                                                                                     1. .292
                                               Tel: 33159472800
                                                             Fax: 33150778598
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Acanthomorpha, Acanthopterygii, Percamorpha, Tetracakatiformes,
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Bernot.A., Fizames.C., Wincker,P., Brottser,P., gaet.er.F.,
Saurin.W. and Weissenbach,J.
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Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14121 of RPC1-98 library from Drosophila melanogaster (fruit AL065629
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Determination of this UAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BOCP).
The BOCP is construction a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitlly.org The BOCP Drosophila melanogaster genome using these BACs. For further information melanogaster genome using these BACs for further information and an official see http://www.fruitlly.org The BOCP Drosophila on the latester de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named ROSWell and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BOCP from the isogenic strain y2; on bw Sp, the same strain used for the BOGP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02.JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                         237 CACTITCAGAAGAAGACAAACAGIAAGCITGGGTTTTTCAGCAGCGGGGGGTTCTCTCAT 295
                                                                                                                                                                                                                                                                                                           229 AAGAACCTCACTITCAGAAGAAGACAAACAGTAAGCTTGGGTTTTTCAGCAGCGGGGGT 288
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                                                                                  17 others
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/db_xref~"taxon:7227"
                                                                                                                                                                     DB 17;
/clone_lib="G"
/note="Genoscope sequence ID
                                                                                                                                                               Score 42.4; DB
Pred. No. 0.33;
8; Mismatches
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/note+"end : T7"
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(**187) 5 * .
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                                                                                                                                                   EST 25-JUN-2002
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BRY_5377 wheat EST endosperm library Triticum destivem CDNA 57 mRNA sequence.
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260 Panama Street, Stantord, CA 94305, USA
7EL: 1-656-325-1521 x 251
Pax: 1-650-325-3748
                                                                                                                                                                                                                                                                                                                                   Clarke,B., Lambrecht,M. and khen,S.
Assessing the utility of Arabidopsis genomic information interpreting wheat EST sequences (Unpublished (2002) Contact: Lambrecht M. The Arabidopsis Information Resource
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/dev_stage="developing endosperm ::ss:c X
(days post anthesis)"
/dote="Vector: Bluesc::pt 1: SK()"
/note="Vector: Bluesc::pt 1: SK()"
/ 271 c 157 q 75 t
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48.4%; Pred, No. 2.3;
tive 0; Mismatches 11c;
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                                                                                                                                                   562 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cultivar-"Wyuna"
/db_xref="taxon:4565"
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An Arabidopsis tuli-length cDNA library was constructed essentially
as reported previously (seki et al., 1998). cDNA cleaved with BamHI
and Khol was liquted to modified Lambda FLC.l vector (Carninci et
al., submitted for publication) digested with BamHI and Sali. This
clone is in a modilied pBiuescript vector. Please visit our web
site (http://www.qsc.riken.go.jp/e/plant/index_e.html) for further
Arabidopsis thallana
Mukaryota, Viridiplantae, Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons: core eudicots:
Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                          1 (bases 1 to 503)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
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ENTGP86TF Entamorba histolytica Sheared DNA Entamoeba histolytica
A2542175
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Coffusion, Van Akreis, and Fraseric.
Determination of clone end sequences from Entamoeba histolytica
HRC LMSS sheared DNA library
HRC LMSS sheared DNA library
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                                                                                                                                                                                                                                                                                                  Confact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4559
Fax: 81-298-36-9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match. 10.7%; Score 38.2; DB 10; Best Godal Similarity 61.6%; Pred. No. 4.9;
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/organism="Arabidopsis thaliana"
/db_xret="taxon:3702"
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Eukaryota: Enturoobidae: Entamoeba
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/clone_lib."RAFL9"
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/clone_lib="bardings">/clone_lib="bardings">/clone_lib="bardings histolytica Shrared DNA*
/clone_lib="bardings histolytica Shrared DNA*
/note="Vector: pHOSI: Site_l: Bst 1: Constructed at The Institute for Genomic Research (TD&A): Rocketlle, Mb.
Genomic DNA isolated from broth cultures of F. Bistolytica using a method described by Clark and Diamond, E.S. (1993) Entamocba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to qive a tight size distribution (-2 kb). The v i i rethod used for the library construction is described in settled for the library construction is described in settled in Smith, H.O. and Venter, J.C. (Making smail insert) in Geneme Sequencing: A Practical Approach, eds. M. Vandin and K. Barell, Oxford University Press, 1999."
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Fukaryota: Metazoa, Chordata: Craniata: Verteliata: File costor:
Mammalia: Butheria: Rodentia: Schurounathi: Muridar: Mirinae: Mus.
Marra, M., Hillier, L., Allen, M., B. Wles, M., Dictrich, M., Duboque, F. Geisel, S., Kucaba, T., Lacy, M., Le, M., Marria, M., Muriss, M., Schellenberg, K., Steptoe, M., Tan, F., Underwerd, K., Morre, F., Thetsing, B., Wylie, T., Lennon, G., Soares, B., Wilson, F., and
                                                                                                                                                                  Clones are derived from the Entamoeba histolytica EMICOMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 GAAGAACCTCACTTTCAGAAGAAGAAGAACTAAGCTTGGGTTTTTTAGCAGACAGT
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                       The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MB 20859, USA
Tel: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashJ-HHMI Mouse EST Project.
Washington University School of Medicinely
4444 Errest Park ParkWay, Box 8501, St. Lodgs
Fax: 314-286-1810
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Entamoeba histolyfica"
/strain="HML:IMSS"
/db_xref="taxon:5759"
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Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                               High quality sequence start: 17
High quality sequence stop: 297.
Location/Qualifiers
                                                                                                       Fax: 301 838 3543
Email: b)loftus@tigr.org
                                                                                                                                                                                                                          Seq primer: M13-Forward
Class: shotgun
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AA914462.1 GI:3053854
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13'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. RNA provided by Dr. Minoru Ko, Mayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Nct I: Site_2: Eco RI; Ist Strand cDNA was primed with a Not I · oligo(dT) primer [5,]
                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 14-MAR-2002
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[ tbases 1 to 520]
Satoh, N., Satou, Y., Kohara, Y., and Shin-i, T.
Expressed acnes in Ciona intestinalis
Unpublished (2000)
               This clone is available royally-free through LLNL; contact the IMAGE Consortium (info*image.llnl.gov) for further information. MGI:684767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 CCCTGCTGTCAGTDTGGCGGTGCCTTCCAGGGCTCCCGAGGCCACACGCTGGGGGTGCT 180
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                                                                                     Seq primer: -28ml * rev2 ET from Amersham
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Ab xret-"taxan:7719"
Artone-"crea@delM"
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Tel: 81-75 753-4681
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                   /tissue_type="mammary_gland"
/dev_stage="4 weeks"
/lab_host="bH168"
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                                                                                                                                                                         /organism-"Mus musculus"
Email: mouseest. wwatson.wustl.edu
                                                                                                          High quality sequence stop: 439.
Location/Qualifiers
                                                                                                                                                                                           /strain-"C57BL/63"
/db xret-"taxon:10090"
                                                                                                                                                                                                                                        /clone="IMAGE:1314471"
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Department of Zoology
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AV845237 AVE Satch unpublished cDNA library, eqs Cicna intestinalis cDNA clone releg08c18 37, mkNa sequence.
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                                                                                                                                                                                                                   158 CCGASCCACACGCTGGGCTGCTGGCTGACGAACATGGTATGTTGCTTTAATTGAGGT_217
                                                                                                                                                                                                                                                                                                                404 AAANTGCCAAGGCTGTGCCAGCAGTAAGAAGAATATGGAATGCAATGCAATTGCAAGAA 463
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                                                                                                                 Score 37: DB 10; Deneth 520;
Pred. No. 16;
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Location/Qualifiers
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/db_xref="taxon:7719"
/clone="rcieq08c18"
                                       r: pBluescript SK*
110 g = 136 t
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94 g 184 t
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
/tissue_type="whole animal"
/dev_stage="egg"
/note="Vector: pBluescript:
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/tissue_type="whole animal"
                                                                                                                                                         0; Mismatches
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/note="Vector: pF
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: Similarity 51.5%;
85; Conservative C
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Contact: Nori Satch
Department of Zoology
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TITLE
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689 bp mRNA linear EST 14-AUG-2002
OGD4410.yg.ab! UG_ABCD1 letture salinas Lactura sativa cDNA clone
BQ868999
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                                                                                                                                                                                   Eukaryota: Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnellophyta: eudicotyledons; core eudicots;
Asteridae; euasterids 11; Asterales; Asteraceae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   belongs to contig QG_CA_Contig2702, see http://cqpdb.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundason Hall, UCD, Davis, CA 95616, USA
Tel: 1-(5.0)-742-1742
Fax: 1-(530-752-9659
Email: akozik/atqc.org [michelmore@vegmail.ucdavis.edu]
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TAG_TISSUE-callus
                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /crqanism-"Lactuca saliva"
/cult.ivar-"Salinas"
/db xref "taxon:4216"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for details.
Plate: QGD4 row: d_column: 10.
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137 c 141 a
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55.5%;
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Phlebobranchia: Clonidae; Clona.
Phlebobranchia: Clonidae; Clona.
J. (bases 1 to 57)
Satob, N., Satou, Y., Kohara, Y. and Shin-i, T.
Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Norl Satoh
Department of Loology
Kyoto University
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Location/Qualifiers
i..571
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/db_xref="taxon:7719"
/clone="rcieg37m02"
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Tel: 81-75-753-4081
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Ciona intestinalis
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	 Human ABC1 transcr	Human ABC1 genomic	Humar, ABC1 gene ex	Nucleotide sequenc	Nucleotide sequenc	Nacleotide sequenc	N.clectide sequenc	Nucleutide Sequenc	Nucleofide sequenc
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Isolated nucleic acid useful for modifying the ATP-binding cassette I (ABCI) and screening for candidate modulatory compounds or substances

WPI; 2002-154404/20.

Human ABCl gene ex Partial human ABCl Human ABCAl homolo	Human polynucleoti Human ATP binding	Human ATP binding	ABCI		ABC1	Human cDNA clone (			Human ABC1 nucleot	Human ABC1 cDNA.	Human ABC1 cholest				ABC1		Human ABC1 gene in	Nucleotide sequenc	ABC1 polymorphism		Human genomic DNA	Human polynucleoti	Human novel protei	Human novel protei	Human immune/haema	Human immune/haema	Human genomic DNA			Human polynucleoti	DNA encoding human
AAD37269 AAS04035 ABA09200	AAK52667 AAU21326	AA170315 AAK51683	AAS06120	AAD37273	AAS06121	AAH07432	AAH18606	AAC69388	AAF83826	AAF92835	AAC69387	AAC69120	AAC69385	AAC69386	AAC69389	AAD37271	AAD37272	AAF25499	AAF93082	AAD16545	AA162954	AA163983	AAD16546	AAD16547	AAK72951	AAK72952	AA162955	AA162956	868	398	AAS33467
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## ALIGNMENTS

Human, ATP-binding cassette 1; ARC1 gene regulation, atherosclerosis; cholesterol metabolism; hypercholesterolaemia; antisense therapy; ds. Rosier-Montus M., Prades C., Lemoine C., Naudin L., Denefle P., Brewer B., Duverger N., Remaley A., Santamarina-Fojo S. Human ABC1 transcription regulatory DNA #2. 96 AAD37266 standard: DNA; 357 02-MAY-2001; 2001WO-EP05488 02-MAY-2000; 2000US-201280P. 21-AUG-2002 (first entry) (AVET ) AVENTIS PHARMA SA. W0200183746-A2 Homo sapiens 38-NOV-2001. AAD37266; RESULT 1 AAD37266 

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Homo sapiens
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                                                                                                                                                                            The invention relates a nucleic acid which is capable of requiating the transcription of human APP-binding cassette I (ABCI) gene, which is a casual dene for pathologies linked to a dysfunctioning of choicesterol metabolism, including diseases such as atheroscicrosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABCI gene. They are used in antisense therapy. Compositions comprising sequences of the invention are used to treat hypercholesterolamia and atheroscierosis. The present sequence is human ABCI transcription revulation in MA.
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Matches 357; Conservative
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15 - MAR - 2000;
23 - JUN - 2000;
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Human ABC1 cholesterol transporter; chromosome 9931; promoter;
ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
cardiovascular disease; coronary artery disease; coronary restenosis;
cerebrovascular disease; peripheral vascular disease;
Alzheimer's disease;
Niuman-Pick disease; Huntington's disease;
Alzheimer's disease;
Frinked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
prognosis; prophylaxis; drug screening; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ø
                                                            Treating a lower than normal high density lipoprotein-cholesterol (HDL-0) level, a higher than normal triglyceride level, or a cardiovascular disease, by administering a compound that modulates LXR-or RXR-mediated transcriptional activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53309
                                                                                                                                                                                                                                                                              The present invention relates to a method for treating a patient diagnosed as having a lower than normal high density to lipoprotein-cholesteroi (HID.-C) level, a higher than normal triglyceride level, or a cardiovascular disease, involving administering a compound that modulates LXF or RXF mediated transcriptional activity or ABCI expression or activity. The LXR gene product may be used in an assay to identify compounds useful for the treafment of a disease or condition selected lower than normal HID cholesterol level, a higher than normal triglyceride level, and a cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 183999 BP; 49549 A; 37944 C; 41170 G; 54950 T; 386 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CCCTGC16TCAGCTCTGGCCGCTTCCAGGGCTCCCGAGCCACGCTGGTGGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TGGAGGTCTCAGCTGAGAGGCTGGATTAGCAGTCCTCATTGGTGTATGGCTTTGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.4%; Score 351.2; DB 22; Length 183999; 98.9%; Pred. No. 1.8e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                            Claim 8; Fig 1; 317pp; English.
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Best Local Similarity 98.99
Matches 353; Conservative
WPI; 2001-244356/25.
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121 CCCTGCTGTCAGCTGTGGCGGTGCCTTGCAGGGTCCCGAGCCACGCTGGGGGTGCT 180

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The invention relates to the human ARC1 cholesterol transporter protein (FBBME2) and to nucleic acid sequences (C69120) Which encode it, ABC1 is a member of the ATP-binding cassette (ABC transporter) superially of proteins, and plays a crucial role in cholesterol mansport particularly cordered in cholesterol trafficking in monocytes and fibriciasts, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is located on chromosome 941, and mutations in this yene are associated with two generic HDD. And density hipoprotein) deticiency disorders, while two generic HDD and familial HDL deliciency (FHA). These diseases of an edistinguishable in that TD is an autosmal remassive disease, while CFHA is inherited as an autosmal dominant trail for everls. The Cquod cholesterolly in the blood correlate with a high risk of caldiovascular disease. particularly coronary artery disease, hut also carebrovascular disease. particularly coronary artery disease, hut also carebrovascular disease. The invention provides quenche most of sease. Compension of HDL has protective effects against cardiovascular disease. The invention provides quenche most networked or cardiovascular disease comprising the administration of an expression of curdiovascular disease comprising the administration of an expression of coronary active fraquent thereof in choosing which mine ABC1 experienced a palator of a palator of a palator of intrinary fraction and methods of general mining for such compounds which mine active transported a palator than an effect internation of an expression and methods of security disease during for such compounds of intrinary disease and methods for determining for such compounds and instead and the compounds of the mineral disease and methods of security disease during for such compounds of the mineral disease comprises of determining for such compounds and formation of disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New ABC1 polypeptide is useful for treating diseases assiciated with.
ABC1 biological activity, e.g. Alzheimer's disease, Bin'thaton's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.3%; Score 340.2; DR 21; Tendin 1054%; 98.9%; Pred, No. 113e 94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 50; Fig 12: 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYBK-) UNIV BRITISH COLUMBIA (XENO-) XENON BIORESEARCH INC
                                                                                                                                                                                                                                                                                  990S-0138048.
990S-0139600.
990S-0151977.
                                                                                                                                                                   2000WO-IB00532.
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Matches 353, Conservative
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W0200055418-A2
                                                                                                                                                                   15-MAR-2000;
                                                                                                                                                                                                                                                                                           08-30N-1999;
17 JON-1999;
                                                                                                                                                                                                                                                                                                                                                                               01-SEP-1999;
                                                                                                                                                                                                                                                   15-MAR-1999;
                                                                                    21 SEP-2060
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atherosclerosis. The genes are useful for developing screening assays to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenosine triphusphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q11. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disorders associated with hypercholesterolemia and
substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein mediated mobilisation of intracellular cholesterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polypeptide. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenosine triphosphate binding cassette protein 1; ABC1; abolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                               181 GCCTGAGGGAACAIGGCAIGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACUTCACT
                                                                                                              241 TICAGAGAGACAAACAGTAAGGTTGGGTTTTCAGCAGCGGGGGGTTCTCATTTTT
                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human ABCl polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product- "ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 122-128; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                          AAF24680 standard; DNA; 10442 BP
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14-SEP-1999;
19-NOV-1999;
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screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and
                                                                                                                                                                                                                                                                        157 CCCGAGCCACACGCTGGGCGTGCTGAGGTGAGCATGGCATGT GGCCTCTCAGCTGAGG 216
                                                                                                                                                                                                                                                                                                                                                             217 TTGCTGCTGTGTGGAAGACCTCACTTTCAGAAGAGAAAAAGAGTAAGCTTGGG119TTCA 276
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                                                                                                                                                                                                       Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein-mediated mobilisation; cholestorol: Tanque: disease;
chromosome 9922-9931; heart disease; hyporcholesterolegia:
                                                                                                                                                        DB 22; Length 10442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adenosine triphosphate binding cassette profein [: AEC];
                                                                                                        Sequence 10442 BP; 2898 A; 2297 C; 2408 G; 2835 T; 4 other;
                                                                                                                                                                                                     41; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCGGGGGTTCTCTTTTTTTTTTTTTTTTTTTTGTTTTTGAGTTGGGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           325 dradernocretaritaterrecidanecrearese 419
                                                                other disorders associated with hypercholesterolemia.
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                                                                                                                                                                                1.2e-38;
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/product= "ABCl polypeption
                                                                                                                                                     44.6%; Score 159.4; Sore 159.4; Score 1surity 81.8%; Pred. No. 1.2e es 184; Conservative 0; Mismatches
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291..7076
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990S-0153872.
990S-0166573.
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08: AAB31365.
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10 AAF2
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tanqer disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9422-9431. The ABCI genes and proteins are diseaful to developing planmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardlovascular disease and
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popul populoctein-mediated mobil hadion; cholesterol: Tangier disease:
chromosome 9922 993: hourt disease: hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         other disorders associated with hypercholesterolemia.
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Pred, No. 1.2e-38;
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323..7108
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81.8%;
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990S-0166574.
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atherosclerosis
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19 - NOV - 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders associated with hypercholesterolemia and alherosclerosis. The genes are useful for developing screening assays to serven for compounds that regulate the expression of genes associated with cholesterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders associated with hypercholesterolemia.
                                                                                                               Adenosine triphosphate (ATP) binding cassette (ABC) polymnoleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 COMBAGGACACACGCTGGGCGTGCTGACGGAACATGGCATGTTGGCCTCAGCTGAGGG 216
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                                                                                                                                                                                                                                                              The present sequence encodes a human adenosine triphosphate (ATP)
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81.8%; Pred. No. 1.2e-38;
Cive 0; Mismatches 41
                                                                                                                                                                                                                     Disclosure; Page 148-154; 215pp; English.
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/*tag= a
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                                      Garvin M;
(CVFH-) CV THERAPEUTICS INC
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Matches 184: Conservative
                                                                            WPI; 2001-137812/14.
                                      Wade D,
                                                                                                                                                                               atherosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                      Lawn RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF24686
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The present sequence encodes a human adenosine triphosphate (APP) binding cassette protein (ABC) | polypeptide, and is isolated from a rangier disease patient. ABCI resides in cell membranes and utilises APP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI gene is localised to chromosome 9922-9931. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated With choicsterol transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 CCCGAGCCACACGCTGGGCGTGCTGAGGGAACATGCCATGTTGGCCTCAGCTGAGG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 ITGCTGCTGTGGAAGACCTCACTTTCAGAAGACAAACAGTAAGCTTGGGTTTTTCA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 ITGCTGCTGTGGAAGACCTCACTTTCAGAAGAAGAAGATGTCAGTGTTACTGGAA 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 10474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10474 BP; 2907 A; 2304 C; 2415 G; 2844 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 GIGGCCIGGCTCTAITTATCTICCTGATCCTGATCTCTGTTCGG 451
/product- "defective ABC1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 GCAGCGGGGGTTCTCTCTTTTTTTTTGTGGTTTTGAGTTGGG
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Best Local Similarity 81.8%; Pred. No. 1.2
Matches 184; Conservative 0; Mismalches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 170-176; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                   990S-0153872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CVTH-) CV THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wade D, Garvin M;
                                                                                                                                                                                                                                         16-JUN-2000; 2000WO-US16755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ademosine triphosphate (AIP) binding cassette protein (ABC) i polynomicotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterclemia and
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Nucleotide sequence of ABCL polypeptide from Tangier disease patient
                                                                        apolipoprofein-mediated mobilisation; cholesterol. Tangle: disease;
Thromosome 942-9431; heart disease; hypercholesterolemia:
atheroselerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F13CTGCTGTGGAAGAACCTCACATTCAGAAGAGAAAAAAGTAAGCTTAGGTTTTCA
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                                                 adenosine triphosphate binding cassette protein 1. Abrl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10474 BP; 2906 A; 2305 C; 2416 G; 2843 T; 4 other;
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                                                                                                                                                                                                                                                                     /*tag= a
/product= "defective ABG1 polypeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ciaim 27: Page 144-150; 211pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garvin M;
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323..7108
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81.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oram JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-US16591.
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990S-0166573
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P-PSDB; AAB31366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN 2000;
                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                      W0200078971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOWEL KM,
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                                                 Human :
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide, and is isolated from a Tangier disease patient. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-Cholesterol metabolism. The ABC1 gene is localised to chromosome 9q22-9q31. The ABC1 denes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of ABC: polypeptide from Tangier disease patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apolipoprotein-mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-9431; heart disease; hypercholesterolem:a; atherosclerosis; cholesterol transport; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; adenosine triphosphate binding cassette protein 1; ABC1;
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GCAGCGGGGGGTTCTCTCTCTTTTCTTTGTGGTTTGGG
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Length 10474;

44.6%; Score 159.4; DB 22;

Query Match

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/note- "CDS does not include stop redia."
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closestere! metabolism; hypercholesterolaemia; antisense terrupy;
exon 18; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acid useful for modifying the Air Binchus cassette I (ABCI) and screening for candidate modulatory conjecusts in substances (\Delta BCI)
                                                                                                                                                                                                                                                                                                           1, HTEFTHITHITHITHITHITETT THE TENTH TO THE TENTH TO THE TENTH TO THE STATE AND THE ANGLE AND THE TENTH TO THE ANGLE AND THE THE TENTH TO THE ANGLE AND THE TENTH TO THE ANGLE AND THE TENTH THE TENTH TO THE ANGLE AND THE TENTH TO THE TENTH TO THE TENTH THE TENTH TO THE THE TENTH TO THE TENTH THE TENTH TO THE TENTH TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 COGREGORACION DE CONTROCTORIO DE CONTROCTO
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Pred. No. 1.2e-38;
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                                              81.8%;
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                                                                  Best Local Similarity 81.8
Matches 184; Conservative
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AAD37269
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Naudin L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roster-Montus M, Arnould-Requigne I, Prades C. Nacdin L
Duvetaer N, Jaye M, Searloss GH, Remaley A, Brower HB:
                                                                                                                                                                                                                                                                                                                                                                   215
                                                                                                                                                                                                                                       100 TTAATGACCAACCAACGACGICCCTCTCAGCTCTGGCCGCTGCCTTCCAGGGCTCCC 159
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Human ABC1 protein, amino acids 1 to 60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, ABC1 gene: atherosclerosis; reverse transport; cholesterol; cardiovascular; neurological; Tangler disease; LCAI deficiency; lecitatin cholesterol acetyltransferase; malaria: diabetes; ss.
                                                                                                                                                                                                                                                                                                                                                            160 GAGCCACACACACTOSACATGCTSGCTGAGGGAACATGCTGGCCTCAGCTGAGGTTS
                                                                                                                                                                                                                                                                                                1 TTAATGA SCAGOSACOGGGG COCTGC COTCAGCTCTGGCCGCTGCCTTCCAGGCTCCC
                                                                                                                                                                                                                                                                          ..
                                                                                                                     Length 159;
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                                                                                                                                                                              Indels
The present sequence is human ABC1 gene exon 18 DNA
                                                     Sequence 159 BP; 32 A; 47 C; 48 G; 32 T; 0 other;
                                                                                                                                              Best Local Similarity 100.0%; Pred, No. 2.5e-39;
Matches 159; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 CIGCTGIGGAAGAACCTCACAITTCAGAAGAGAGAAACA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.5%; Score 159; DB 24;
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Lemoine C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS04035;
                                                                                                                        Query Match
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AAS04035
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Hulliate polyticistics, do SEC 1D for 2196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; ceil differentiation; arowth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and charmon at all
transport of cholesterol. The nucleic acids and polypepides are also useful for treating and preventing cardiovascular and neurolealical pathologies, and other diseases e.g. Tangler disease, lecitiin-cholesterol (LCAI) deficiency, malaria and diabetes.
                                                                                                                                                           PETECTGCTGGGAAGAACCCACTTTCAGAAGAAGAAAAATGTGAGCTGTGGTGGAA 268
                                                                                                                                              97 CAGITAATGACCACGGCGTCCCTGCTGTGTCGCCGCGCCTTGCCTTGCCTTGCCTTGCTTGCTT 156
                                                                                                                                                                                                157 POGGAGGCACAGGCTGGCGTGCTGAGGGAACATGGCATGTTGACTTGAGG 216
                                                                                                                                                                                                                                                1: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human proteins and DNA encoding sequences useful for prevention, freating or ameliorating a medical condition in a man asset service?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       haematoporet of disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell culture; drug screening; gene therapy; attructaments;
antiasthmatic; antiarthritic; haemostatic antiarrerus; erotuc;
cytostatic; osteopathic; vasotropic; cardian; vincin se artibue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis; coronary heart disease; arterial iscuargia;
bone disorder; osteoporosis; vascalar growth disorder;
tissue regeneration; wound healing; intection; trenge disorder;
                                                                                          40.8%; Score 145.8; UB 22; Length 446; 80.9%; Pred, No. 4.9e-35;
                                                                                                                    47; indels
                                                                                                                                                                                                                                                                                                   277 GCAGCGGGGGTTCTCTCTTTTTTTTTGTGGTTTGAGTTGGG 521
                                                                                                                                                                                                                                                                                                                 269 GIGGCCTGCCTCTTTATCTTCCTGATCTCTGATCTTGTTGGG 333
                                                                Sequence 446 BP; 96 A; 123 C; 112 G; 115 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human AHCAl homologue-encoding cDNA, SEQ ID NO:975.
                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antifungal; vulnerary; antiulcer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                             ABA09200 standard; cDNA; 7086
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27-APR-2000: 2000US-0560875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. arthritis and cancer
                                                                                                                    Matches 182; Conservative
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                                                                                                        Best Local Similarity
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                                                                                          Query Match
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nuclectide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nuclectides or polypeptides in a sample, and methods of detecting the nuclectides or polypeptides in a sample, and methods of indentifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell afferentiation activities; stem cell growth factor activity; haematopolesis requiatory activity; tissue growth activity; immuncomodulatory activity; or inhibin related activities;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                              Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABBA08225-ABB09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombotic or thrombotic or thrombotic or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or qene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., astuma or arthritis), proliferalive reticopathy, atherosclerosis, coronary heart disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
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(i) Mismatches 42; Indels
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Claim 1; Page 833 835; 1963pp; English.
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AAK52667;
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              cell proliferation: cell differentiation: gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                     Ma Υ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: Records for SEO ID NO 2110 (AAK5258.), 2111 (AAK5282) and 4666 (AAM80020) are omitted as the relevant pares from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine; peptide therapy; stem cell growth factor, Laematopolesis;
tissue growth factor; immunomodulatory; cancer; leskacmia;
nervous system disorder; arthritis; infiammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                     V, Zhou F, Xo C, Cao Y,
Ren F, Chen R, Wang aWi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>:</u>
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1.7e-34;
.hog 42; indels
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Xue AJ, Yang Y, Wejbrman T, Goodrich R:
                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT, Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 4558-4560; 6221pp; English.
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2000US-0693325.
2000US-0728422.
                                                                                                                                                                                                                                            2000US-0598075.
2000US-0620325.
                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098.
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                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                       WG200157190-A2.
                                                                                                                                                                                                                                            20-JUN-2000;
19-JUL-2000;
                                                                                          Homo sapiens
                                                                                                                                                                                                               03-FER-2000;
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                                                                                                                                                                                                                                                                           01-SEP-2000;
15-SEP-2000;
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30-NOV-2000;
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                                                                                                                                                                                   Human: ATP bisding cassette transporter 1; ABC1; coronary heart disease; defranciological; atheroscierosis; cardiovascular; inflammatory disease; psoriasis; lipid disorder; antibacterial; septic shock; gene therapy; immunosuppressive; lupus erythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to four common polymorphisms in the gene encoding ATP-binding describe transporter 1 (ARCI). ARCI is associated with decreased Apod-3 mediated efflux of cholesterol. The polymorphisms in ABCI directly affects cellular lipid homeostasis, which is a key factor in the atherogenetic processes. The ABCI polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular diseases (coronary heart disease, atherosclerosis) and inflammatory diseases (psortasis, lupus crythematosus). The Identification of ABCI as a transporter for interleukin-libeta (IL-libeta) identifies this gene as a candidate for treatment of inflammatory diseases including rheumatoid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis and septic shock. The present sequence is human ABCl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New adenosine triphosphate binding cassette transporter-1 gene polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
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                                                                                                                                                  Human ATP binding cassette transporter 1 (ABC1) gene.
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80.9%; Pred. No. 1.7e-34;
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                                   AAD21326 standard; DNA; 7260 BP
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Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     ATP binding cassette transporter 1: ABC1; human: lipid disorder; cholesterol; cardiovascular disease; inflammatory diseases; antifammatory diseases; antibaconduc; antibaconduc; dermatorological; Tangier disease; coronary heart disease; disquosis; gene therapy;
                                               277 GCAGCGGGGGTTCTCTTTTTTTTTTGTGGTTTTGAGTTGGG 321
                                                                       405 GTGGCCTGGCCTCTATTATCTTCCTGATCTCATCTTTTGG 449
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AAI70315
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polymorphisms alter the amino acid sequence of ABC1 and therefore may affect its function. The 2 most common polymorphisms (G596A) and A2589G) are both associated with a decreased in vitro AppA-1 mediated efflux of cholesterol from mononuclear phagocytes, a feature typical of Tangier disease. 3 of the variants (G596A, A2589G and G3456C) are significantly increased in a population of men having low high density lipoprotein-cholesterol levels and established coronary heart disease (CHD) relative to CHD-free control subjects. The use of the provided ABC1 polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular chiseases, and inflammatory diseases (e.g. psoriasis, lupus erythematodes) is claimed. Modulation of ABC1 transcripts or proteins by antisense or ribozyme technology or RNA decoys is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 CAGTIAATGACCAGCCACGGGGGTCCCTGCTGTCAGCTCTGGCCGCTGCCTTCCAGGGCT 156
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Matches 182; Conservative
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Copyright (c) 1993 - 2003 Compugen Ltd.
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May 9, 2003, 11:17:01; Search time 10:66.33 Seconds (Without alignments) 9746.207 Million rell updates/sec 1 tggaggtctcagctgagagg.......gagggaaggaaggaagctgtate 4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues Post-processing: Minimum Match 0%
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Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-09-846-456-2 357 Title: Perfect score: Sequence: Scoring table: Searched: Run on:

em\_vi:\*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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7	346.2	95.	201144	J 1			AF287262	Homo sapi
	2.17.2		96906	7 5			AC021345 AE258624	Homo sapi
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LOCUS		AX351030			357 bp	DNA lin	inear PAT	PAT 06-FEB-2002
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VERSION			1 61:18	:18616	386			
SOURCE	human	an.						
ORGANIS	Σ	Homo sapiens Eukaryota; M Mammalia: Fu	ens : Metazoa; Eutheria:		Chordata; Cran	aniata; Vertebrata; tarrhini: Hominidae		Futeleostomi; Homo
DEFERENCE					,			

Rosier-Montus,M.F., Prades.C., Lemoine.C., Naudin.L., Denefle.P., Brewer,B., Duverger,N., Remaley,A. and Santamarina-Fojo.S. Regulatory nucleic acid sequences of the abol gene

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Santamarina-Fojo,S., Peterson,K., Knapper,C., Gli.y., Freeman,L.,
Cheng.J.F., Osorio,J., Remaley,A., Yanux,R., Bandenschild,C.,
Prades,C., Chimini,G., Blackmon,E., Francols,T., Buverqer,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson, F.S. and Brewer,H.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Santamarina-Pojo,S., Peterson,K.M., Knapper,C.L., Freeman,L.A., Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackmon,E.E., Francols,T.L. and Brewer, H.B. Jr.
Direct Submission
L. Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heart, Lunq and Blood Institute, Bethesda, MD 20892, USA
Location/Qualifiers
I. 149034
//Dranism-Homo sapiens"
//db.ref-*taxon:9606*
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Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
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Homo sapiens ABCAl (ABCAl) gene, complete eds.
AF275948
Patent: WO 0183746-A 2 08-NOV-2001;
Aventis Pharma S.A. (FR)
Location/Qualifiers
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ARLSBERHLLLYSWONTSWEDMRYUFTLLOOIKKSSSNLKI, JUFILVUNETFSGELYH
NISSLPRSTVDKMLASWONTHKVFLQGYQLHLTGL.CNGSKSEEMIGULROOFVSELUGI.
.40473,45012.
25989,40385.
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/db_xref+"G1:9247086"
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1674,25831.
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4998. . 5270
/rpt_family "Als"
5563. . 5839
/rpt_ramily "Als"
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[2810], .12902
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25038. .25314
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4240. .4509
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15220, .15399
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15508. .15787
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18660. .18860
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8800. .9046
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9998, .10279
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join(1454, ...1674,
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20950, .21206
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GWKLTOOQFWALLWKRILLIARRSRKGEFAQIVI. PAVEV. TAIVESTIVPPEGKYPSLE
LQPHYNDOTFVSNDAPEDTGTLEH NAJKDPPETT, KYMENNE IPDI PCOAGEEBW
TAPVPQTIMDLEQNGNWHYNDISPERTOGSSSUS, IKMI PEVE HGAGGEPPEDKKNITA
DILODLTGRAI SDYLWTYVO I JAKSIKNK IWVNE PEVGT SSG GVSKTOAL PSOGEVN
DAXKOMKKHLKLAKDSSADRFINSLGFFFFTGLD FENNVKVE NWKGWHAI SSFINVIN
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AVDGLALNFYEGQITSFLGHNGAGKITTMSILTGLFPPTSGTAYIIGKDIKSEMSTIR
ONLGVCPOHNVLFDMLTVEEHIWFYARLKGISEKHVKAEMEGMALLVGLFSKLKSKT
                                                                                                                                                                                                                                                                                                                                                  SQLSGGWQRKLSVALAFVGGSKVV11,DEPTAGVDPYSRRG1WELTLKYRGGRTT11,ST
HHMDEADVLGDRIAITSHGKLCCVGSSLFLKNOLGTGYYLTLVKKDVESSLSSCRNSS
STVSYLKKEDSVSGSSSDAGLGSDHESDTLT1DVSA1; SNLTRKHVSEARLYED1GHEL
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RASTVYELIQBRUSKAKHUGH SGVKRYIYWLSNEVWIMSTONVVPATLUITETFUG
KSYVGSTNLPPLALLLLLYGGKITPLMYPASFVFK IBSTAVVLTSVNLFIGINGSVA
TFVLELFTDNKLNINDILKSVFLIFPHFUGGGILIBVKNANJAMADALERFGENREVS
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RILDGGGONDILEIKELTKIYRRKRYAVDRICVA, IFPSETFGILGVNGAGKSSTFKM
LTGDTTVTRGDAFLNXNSILSNIHEVHONMGYCPQFDATTELLTGREHVEFFALLKGV
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BEKRREFHAWALSVYKEGKSVVITFHSMEEGEALATHWA IMMORFRELGSVOHLK
NRFORGYTIVVRLAGSNPDIKPVODFFGLAFPGSCANTHWIGYOLPSSLSSLARI
FSILSOSKKRLHIEDYSVSGTTLDQVFVNFFAKNOGSTSHILKGISLHKNOTVVDVAVIT
                                                                             QQLDGLDWTAQDIVAFLAKHPEDVQSSNGSVYTWRFAFNET NÇAJRI ISRFMECVNLN
                                                                                                                              NKIKDGYWDPGPRADPEDMRYVWGGFAYLQDVVEQA I IRVLIGFEKKTGYYMQOMPY
PCYVDDIFLRVMSRSMPLFWILAWI YSVAV I IKGI VVEKŁARI KETMRIMGI DNS II,M
                                                                                                                                                                                                              SRANLAAACGGTTYFTLYLPYVLCVAMGDYVGFTLKTFAXLLSPVAFGFGCEYFALFE
EQGIGVQMDNLFESPVEEDGFNLTTSVSMMLFDTFLYGVMTWYTEAVFPGGYGTPPPW
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYVLPYEAAKEGAFVELFHEIDDRLSDLGISSYGISET FLEEI FLKVAEESGVDAETS
DGTLPARRNRRAFGDKOSCLRPFTEDDAADPNDSEI 10FESKETFLLSGMDGKGSYQVK
                                                RQVMAEVNKT FQELAVFHDLEGMWEELSPK I WTFMENSQEMIELV FMILLDSRUNDHFWE
                                                                                                          KLEPIATEVALINKSMELLDERKFWAGIVFTGITPGSIBLEHHVKYKIRMDIDNVERT
                                                                                                                                                                                          FSWF1SSLIPLIVSAGLLVV1LK1GNLLPYSDPSVVFVF1.SVFAVVT11,QCF1,1ST.,F
                            GGNGTEEDAETFYDNSTTPYCNDLMKNI,ESSPI,SRI,TWKALKPI,J,VGKILYTPDTPA
SWSDMRQEVMFLTNVNSSSSTQIYQAVSRIVCGHPEGGGLKIKSUNMYEDNNYKALE
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37999, 3816
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36167, .36440
/rpt_family="Alu"
37617, .37892
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50547, 50614
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38995, 39271
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1547, .41565
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11657, 41670
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18473. .48669
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54285, 54410
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/rpt_family-"Alu"
:1692. .31973
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54849. .54988
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14349. .44626
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55029. .55226
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Futelesstori;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Hoss:
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Haydon, M.R., Brooks Wilson, A.R., Pimstone, S.N. and Chee, S.M.
Compositions and methods for modulating hdl choicsteroi and
trid, year delevels
Patent: WO 0115676-A I 08-MAR-2001;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 480)
                                                     Direct Submission
Submitted (07-JAN-2000) Porsch-Oezcucrupemez M.K., Institute for Clinical Chemistry, University of Regensburg.
Clinical Chemistry, University of Regensburg, GERMANY
Franz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
Location/Qualifiers
                                                                                                              181 GGCTGAGGGAACATGGCATGTTGGCCTCAGGTTGGTTGTTGTTGTTGTAGAAGAAGTTGTTGTT 240
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/gene="ABC-1"
/function="cholesterol efflux regulatory protein"
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/db_xref="taxon:9606"
/chromosome="9"
/map="9931"
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Porsch-Oezcueruemez, M.K.
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Direct Submission of 12000)

Reflectly A. Submission 2001) Sanger Centre, Hinxton, Campridgeshire, CB10 15A, UK. E-mail organizes: humquery@sanger.ar.ux Cloneraques/Sanger.ac.ux

CB10 15A, UK. E-mail organizes: humquery@sanger.ar.ux Cloneraques/Sanger.ac.ux

On Jun B. 2001 this sequence version replaced di:14272250.

During sequence assembly data is compared from overlapping clone name white that the variation amountation may not be found in the sequence submission or corresponding to the overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with sonly a small overlapping clone, as we submit sequences with sonly a small overlapping clone, as we submit sequences with an alternate chemistry or covered by high quality data (i.e., phich quality >> 30); an altempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. FMHLS. Switcher assembly was confirmed by restriction digest. The following a database can be found at at.
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Human DNA sequence from clone RPII-31J20 on chromosome 9, complete
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Mammalia: Euthoria: Primates: Catarrhini: Hominidae: Homo.
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/product "All binding cassette transportor 1" /profession "AC21428.1" //de xroft" [124034.2] //de xroft" [124034.2] //de xroft" [124034.2] //de xroft" [124034.2] //de xroft [12
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U: Mismatches 3
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Matches 35% Conservative
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7496. 2714
//octe=*MIR repeat: matches 12. 250 o: Cousensus
//octe=*MIR repeat: matches 6. .128 of consensus
//octe=*MIR repeat: matches 6. .128 of consensus
//octe=*Limb repeat: matches 5696. 5821 of consensus
//octe=*Alusg repeat: matches 1. .295 o: consensus
//octe=*Alusg repeat: matches 6040. .617 o: consensus
//octe=*Limb repeat: matches 6040. .617 o: consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20957. 21107

// Anote="MIR repeat: matches 49. 212 of "Gransus" 21783. 22078

// Anote="MIR repeat: matches 7. 302 of Consensus" 22320. 22439

// Anote="MIR repeat: matches 10. 146 of Consensus" 22533. 22839

// Anote="Alusx repeat: matches 1. 307 of Consensus" 24245. 23454

// Anote="Alusx repeat: matches 2137. 2750 of Consensus" 24245. 24544

// Anote="Alusy repeat: matches 2. 302 of Consensus" 2455. 24544

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// Anote="Alusy repeat: matches 2. 302 of Consensus" 24556. 24544

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// Anote="Alusy repeat: matches 2. 302 of Consensus" 24556. 24568

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// Anote="Alusy repeat: ma
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10957. .21107
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2649. 26892
/note="11 copies 4 mer tata 81% conserved"
27998. 28103
/note="MIR repeat: matches 28. .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1828. 1877
/note="L2 repeat: matches 2649. 2698 o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3145. .8434
Inote-"AluSc repeat: matches 1. .298 ct
12145. .12713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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1358. .1653
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// 101256. 40334 repeat: matches 5774. .6331 of consensus. 40256. 40334
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/hote-*LTRIGA repeat: matches 6, .450 of consensus" 45359, .45486
//hote-*MIR repeat: matches 1, .139 of consensus" 46654, .46693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note, "L2 repeat: matches 2625, .2710 of consensus"
49578, .49758
                                                                                                                                                      31987, 32116
Anote: MRESA repeat: matches 60, .188 of consensus.
32450, .32536
Anote: MRESA repeat: matches 14, .106 of consensus.
33293, .33380
                                                                                                                                                                                                                                                                           74435, 34588
760te+"MFR5A repeat: matches 13, 189 of consensus"
34729, 34473
760te-"Mik repeat: matches 49, 198 of consensus"
35802, 35951
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50:189, .50347
                                                //corles-MHR report: matches 2. .245 of conscisus...
30121. 30422.
//noter.malusq repeat: matches 1. .302 of consensus...
31424. 31734
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47118 47429
/note="Alusx repeat: matches 1, 312 of consensus"
47915, 48883
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74054. $5012
7405e-"Alusp repeat: matches 1. .302 of consensus" $5002. $5343
                                                                                                                                    /note-"Alusp repeat: matches 1. .308 of consensus" 31987, .32116
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56238. .56286
7.00te="H8 copies 3 mer tgt 72% conserved"
56342. .56673
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                                                                                                                                                                                                                                                                                                                                                                                       Zhote "MJR repeat: matches 77. .248 of crusensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"MIR repeat: matches 30, .185 of consonsus"
42010, .42194
               .129 of consensus"
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Zhote**MIR repeat: matches 9. .188 of consesus*
49847. .49873
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                                                                                                                                                                                                                                                              /note+"22 copies 4 mer atgg 79% conserved"
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54337. .54544
               Z8985, .29213
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Conomo

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Lebbezky, J., Thou, T., Jacke, K., Macdonald, P., Marquis, N., McEwan, P., Methik, A., McHuan, K., McLaghlin, J., Weldigoll, McGris, J., Referson, K., McLaghlin, J., Weldigoll, McGris, J., Berceson, K., Sultan, V., Stanger, Towns, R., Santos, K., Severy, E., Stanger, Domann, N., Stojanovic, N., Subramanian, A., Tokanger, J., Stanger, Domann, N., Stojanovic, N., Subramanian, A., Tokanger, J., Verker, E., Teretr, A., Voskillev, H., Vo, A., Wheeler, J., Wu, X., Birect, Skip, J., Stoph, Cambridge, M., Ord, J., Kheeler, J., Wu, X., Chrest, Skip, J., Skip,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead lustitute/ MIT Center for Gegore Research Center code: Wids
Web Site: 17:19//www.seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M1: M78415; 100% of reads chemistry: Dye-terminator Eng Dye; 100% of reads chemistry: Dye-terminator Eng Dye; 100% of reads Asserbly producing: Phtap: version 0.96073 consensus quality: 11/571 bases at least Q40 consensus quality: 11/571 bases at least Q40 consensus quality: 160940 bases at least Q20 linear size: 1850%; agarose tp linear size: 1850%; agarose tp linear size: 17/244, sum off-contigg quality coverage: 2.9 in Q20 bases; sum of-contigg quality coverage: 2.9 in Q20 bases; sum of-contigs
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1134 2543; contig of 1531 bp in length
1635 2743; app of 100 bp
2735 4415; contig of 1681 bp in length
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contiq of 1270 bp in length
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12254; everiq of 2467 bp in length
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28184: contig of 2377 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 100 bp
contiq of 1994 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34399: gap of 100 bp | 3818: contig of 3919 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 2831 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17201 17300: gap of
17301 20141: con
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31338: com
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4516 5785; con
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5886 7879; cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG 22-APR-2000
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Homo sapiens clone RP11-1M10, WORKING SRAFT SFUJENCE, 39 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DD 120580 IGGAGGTCTCAGCTGAGAGGCTGGATTAGCAGTCCTCATTGGTGTATGGTTGTAGAGA 126521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa: Chordata, Craniata, Vertebrata: Euroleostomi;
Mammalia: Eutheria: Primates; Catarrhini: Homin:dae; Homo.
1 (bases 1 to 175064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D 120461 CCCTCCTGTGAGCTCTGGCGCTCCTCCAGGGCTCCCGAGCCA'ACA'AGACAGGCTTCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCCTGCTGTCAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGGCCACACACT 1830GTGCT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-MERSA repeat: matches 15, .72 of monseus.s. 65043, .65341
/note-*Alusx repeat: matches 1, .295 of consensos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 TCTTTGTGGTTTTGAGTTGGGGATTGGAGGAGGGAGGGAAGGAAGGAAGGTG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSx repeat: matches i. .306 of persensus"
        /note="AluSq repeat: matches 1, , 411 of enhancesus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.3%; Score 340.2; DH 9; Louth (25408; Harity 98.9%; Pred. No. 2.6e-50; Conservative 0; Mismatches 3; Indels 3; c
                                                                                                                                                                                                                                                                                                                                                                                                                         'note-"16 copies 4 mer atat 68% conserved,"
                                                                                            .272 - 0:
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/note="MERSA repeat: matches 72, .186 of
                                                                                                                                                                                                              63991. .64159
/note="MIR repeat: matches 78. .244 of m
64590. .64651
/note="12" copies 2 mer ta 70% conserved"
64593. .64656
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                                            59443. .60004
/note-"L2 repeat: matches 2088.
60201. .60355
                                                                                                                                                                           /note-"MIR repeat: matches 20.
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Homo sapiens, clone RP11-1M10
Unpublished
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AP287262 201144 bp DNA Libear FR: 29-APR-2001 Homo Sapiens ATP Eliding cassette Lsub-family A member 1 (ASCA) and SNAP protein genes, complete cds. DD 151511 TGGAGGTCTCAGTTGAGAGGCTGGATTAGCAGTCGCTGGTTGGGGGTTTTTGGAGG 151452 35 151451 AFAACTGATGGTGGTGGTGCGCGCGCGGTTTCAGTTAATGACGAGCAGCAGCAGGTT 151393 by 121 cociertoreascrictiscoactiechtricassectecesasceacacteseserost 30 DE 151392 cocrectistascrictisectectereascascecesescasceactes 313 S DE 151272 THEAGAGAGAGAAAGATAAAGTTGGGTTTTTTCAGCGGGGGGGTFTTTT 151233 THEFT THE THEFT THE THEFT THE THEFT THE THEFT THE THEFT THE THE THEFT TO THE TREE TO THE TREE THE THEFT THE THEFT THE TREE TABLE THE TREE TABLE THE THEFT THE TREE TABLE TABLE THE TREE TABLE THE TREE TABLE THE TREE TABLE THE TREE TABLE TABLE THE TREE TABLE TABLE THE TREE TABLE THE TREE TABLE THE TREE TABLE THE TREE TABLE TABLE THE TREE THE TREE TABLE THE TREE Homo sapiens Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutelesstom: 181 GUCTCACOGAANATGCCALCTTGCCCTYAGCTGAGGTTGCTGCGCAAAAAAAACT 240 61 AIAACTGAIGSTIGCTIICGCCTGCTGTTIATGTTTCAGTIAATGAGGAGGGAGGGGGTGI 126 Salis 1 TOGAGSTOTCAG/TGAGAGGGCTGGATTAGGAGTCCTCATTGGTGTATGGCTT130AGCA 60 Length 12 Cond; 3; Indels 95,38; Score 440,2; DB 2; 98,98; Pred. No. 2,7e-90; 2.5588. 25707 /cote-"assembly\_fragment" 25808. 28184 /no.co-"assembly\_fragment" 28285. 31318/\_fragment" 1439. 34239 /note-"assembly\_fragment" 34400. 38318 /note-"assembly\_fragment" 34419- 42835 70.0 e assembly tragment 48217 (526.8 / 700 e assembly tragment (22) e assembly tragment 5693 (5693 (568) / 700 e assembly\_tragment 597.8 (6.86) / 700 e assembly\_tragment 5762 (6.86) U: Mismatches 88419. .42835 /note="assembly\_fragment" 42936. .45448 42936. .45448 /noter"assembly\_fragment" 45649. .4816 /note:"assembly\_tragment" 68538. 71458 /note-"assemtly fragment" 68538. 71458 --/note-\*assembly\_fragment vector\_side:lett\* 71559, 76888 AF287252 AF287262.1 GI:13876612 offane\_end:SP6 Matiches 35%; Conservative Homo sapiens. Query Match Best Local Similarity nisc feature misc\_feature misc\_teature misc\_feature mise\_featare misc\_feature misc\_feature mīsc\_feature misc\_feature misc\_feature misc\_feature misc\_feature misc feature misc\_feature misc feature LUCUS DEFINITION ORGANISM ACCESSION VERSION KEYWORDS SOURCE KES:31.7 AF287262 õ ó ŝ ć

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KSPYSSTNLPVLALLLLYGWSTTPLMYPASFVFKIPSTAYVUTSVNLFTGTNGSVA
KPYSSTNLPVLALKSVYLLFPHFCLGGRIDDWYROMADJAFFFSDENDSVA
PLSWDJNGRNLFAMYNCKYVFFLITVLQYRFFTRPRPRVAKISPIANDFDEDVRRFVS
PLLIGGGGONDILLETKELTKIYRRKRRPANDRLCVGIPPGECFGLLISVNGAGSKSSTFKN
                                                KLEFLATEVWI, INKSMELLDERKEWAGIVFTGITPGSIELPHPVKYK I RMDJ DNVERT
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SEPPEGAPEGHFPURAMPSAGTLPWVOGITORAMUCFRYPTFGEAGVVGRENKSIV
ARLFSDARRLLLYSOKDTSMCDMRVLRTLQQIKKSSSNLKLODFLYDNETFSGFLYH
NLSLDRSTVDKHLRADVILHKVFLQYQIKKSSSNLKLODFLYDNETFSGFLYH
KEKLAAERVLTRSNDJILKPILRYTCQYQLHLTSLCNGSKSEEMIOLGODGOSEJCGLF
KEKLAAERVLTRSNDJILKPILRYTSTSPFPSKELAEATKTLLHSLGTLAGELFSNR
SWSDNRGEWPWLTNWNSSSSTGYIQVOKSRIVGHPFGGGGLKTKSLMWTENDNYKALF
GGNGTREDAETFYDNGTTPYCNDLKRNLESSFLSRIWKALKFLLYFDTPAT
RQVMAEVNKTFQELAVFHDLEGMMEELSPKIWTFMENSGEMDLVRMLLDSRDNDHFWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (13-JUL-2000) Genome Science Department, Lawrence Berkeley National Laboratory, 1 Cyclotron RJ, MS 84-171, Berkeley, CA 94720, USA
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/gene-"ABCA1"
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 201144)
010.7.. Caveller.L. Chiu.S., Yang,X., Rubin,E. and Cheng,J.F.
Human and mouse ABCAl comparative sequenching and transgenesis
studies revealing novel regulatory sequences
21251004
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/gene-*ABCA1*
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Qiu.Y., Cavelier,L., Chiu,S., Rubin,E. and Chenu,J.-F.
Direct Submission
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/organism="Homo sapiens"
/db_xref="taxon:9606"
33931. .181457
/gene="ABCA1"
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Dupus Ising Andrews 1 to $6698)

Bitton, B. Listow, L. Nusbaom, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwith, J., Barnain, Beckerly, R., Heda, F., Anderson, S., Baldwith, J., Barnain, Beckerly, R., Heda, F., Bodyskiy, L., Howkhaller, B., Brown, A., Barkett, G., Gastie, A., Chocpel, Y., Colandelo, M., Collins, S., Collymore, A., Tooke, F., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferretra, P., Fitzhudi, W., Forrest, C., Gage, D., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Labors, R., Heaford, A., Horton, L., Howland, J.C., Labors, C., Lieu, C., Liu, S., Locke, K., Maydond, J., Maydon, B., McGurk, A., McKentas, A., McMand, J.C., Waldrim, J., McDues, L., Mortow, J., Mytor, J., Norman, C. H., O'Connor, T., O'Connell, P., Olivar, T.M., Feterson, K., Pitzhani, C., Pollara, V., Raymond, C., Riley, B., Schuck, R., Scher, P., Spencer, B., Stanger-Thomann, N., Subramanian, A., Talamas, J., Testaye, S., Theogyse, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Mu, X., Washin, D., Ye, W., J., Charles Stron, Research, 420 Charles Strond Institute/MIT Center for Cenvane Research, 420 Charles Strond Cambridge, MA 02141, 38A
                                                    HTG 13-JUL-2000
                                                                                                                                                                                   Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases i to 96698)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens clone RP1: 24J9, LOM-PASS SEQUENCE SAMPLING:
AC021345
AC021345, G1:9130845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This record contains 92 individual sequencing reads that have not been assembled into contigs. Huns of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L4483
                                                      linear
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4816: contig of 914 bp in length
5: qap of 100 bp
5759: contig of 843 bp in length
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                                                                                                                                                                                                                                        Birren,B., Linfon,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RPI: 24.19
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                        DNA
                                                    dq 86906
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2824: con
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3802: con
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/gene="ABCAl"
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140179. .14
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Homo sapiens ATP binding cassette transporter 1 (AMCA1) gene, exon
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Pullinger(C.R. Hakamata, H., Duchateau, P.N., Eng.C. Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
Analysis of hABC1 gene 5' end: additional peptide sequence, promoter region, and four polymorphisms
Biochem. Blophys. Res. Commun. 271 (2000) In press Pullinger(C.R., Hakamata, H., Duchateau, P.N., Eng.C., Aouizerat, B.E., Fielding, C.J. and Kane, J.P.
                                        13050 CCCTGCTGTGAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCAAAAC301GGGAGTGCT 12991
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/db_xref-"taxon:9606"
/chromosome-"9"
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Mammalia: Esthesia: Primates; Catarrhini; Hominidae: Homo.
1 (bases: Lo. 10442)
Lawu, K.M., Wade, D., and Garvin, M.
Rawulario: With binding cassotte transporter proteir abil
Patent: Word-8724 A. 18-DEC-2000;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Lawn, R.M., Wade, D., Ordr. J.F. and Carvin, M.
Alp binding cassette transporter protein abol polypeptides
Patent: Wo 1078971-A L 8-DEC-2000;
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Location/Qualifiers
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/organism="Homo sapiens"
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ACKADIO/ 1042 bp MRNA Linea: FET CY-AUG-2005 HOMO Sapiens AIP-binding cassette transporter [ (ABCAL) MENA, COMPLETE Cds.
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SYPPYEQHEGHEPNKAMPSAGTIPWYGGIGNRNSSNLYAFPGEAPGYVGNFNKSIV
ARLESDARELLYSQKDTSMKDMRKVLRTLGOFKNSSNLYAKLOPFLVDNETFSGFLYH
NLSLENKSTRLLLYSQKDTSMKDMRKVLRTLGOFKNSSNSEENJOLGOFLVDNETFSGFLYH
NLSLENKSTVDKMLRADVILHKYFLGOFYGHTTSLCNSKSEENJOLGODGVSELGGLP
KEKLAAAERVLRSNMDILKPIGATGLTSLCNSKSEENJOLGODGVSELGGLP
SWSDKROEVRELTNNNSSSSTOIYOAVSRIVCGHPEGGGLKIKSLNWYEDNNYKALF
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ROVMADVNRTFOGLAFFDLICHMEELSPRITTMTHENSCHALLDSRINDHFWE
QQLDGLWTAQDIYARFAKHPEDVQSNGSYTWREAFNETHOAIRTRSRINDHFWE
CQLDGLWTAQDIYARFAKHPEDVQSNGSYTWREAFNETHOAIRTRSRINDHFWE

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VCYDDIFTRWSRSWDLEWTLAMIYSSYNIIKGIVEREREHKETMR MGLDNSIIW
FSWFISSLIPLLVSAGLLVVILKGNILLPYSDPSVVEYFLSVFAVVILGCFIISTLE
SRANLAAACGGIIYFTLYLDYVLCVAWQDYVGFTIKIFASILSPVAFGGEFYFALFE
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AVDGLALNFYEGOITSFLGHNGAGKTTTMSII.TGLFPPTSGTAYILGKDIRSEMSTIR
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SQSGGWGKKLSVALAKPGGSKVVLDDEPTACVDPYSRRJ IWELLLKYRQGRTTILST
HHWDEADVLGDR1AT1SHGKLCYGGSSIFLKNQLGTVYTTLYKKDVESSLSSCRNSS
STVSYLKKEDSVSQSSSDAGLGSDHESDT.11DVSA ISNITRKHVSRARLVEDIGHEL
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Porter J.G., Seilhamer, J.J., Vaughan, A.M., and Pram, J.F.,
Direct Submission
Submitted (Ge-JUL-2000) biscovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Pajo Alto, CA 94304, USA
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ABCAl gene expression and apoA-1-mediated choles: ero. efflux are
                              217 TIGCIGCTGIGGAAGAACCICACTITCAGAAGAAGAAGAAGAAGIAGIAAAGTIGGGIGTITGA 276
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/product="ATP-binding cassette transporter |" /protein_id="AAF98175.1" /db_xref="G1:9755159"
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/db_xref-"taxon:9606"
/chromosome-"9"
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LOPWMYNEUYTEVSNDAPEDTGTLELLNALIKDPGFGIRCMEGNPJPDTPCVAGEEFW
TTAPVPGITMILIGURISWFMQNPSPACQCSSDKIKKMLFVCPPGAGGLPFFORKONTA
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TPVLELFTENKLINNI NOELKSVELIFPHFCLGRGLIDMYFNGAMADALERESFNFYS
PLSWELVGKNI,FAMAVEGVVFFLJTYLLQYRFFIRPPRYVAKLSPLNDEHSIVYREBRU
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SELQJSKVKESYV*
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Mammalia: Eutheria: Primates, Catarrhini, Hominidae, Homo.
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Hammalia: Eutheria: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 10474).
Lawn.R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abcl polypeptides
Patent: Wo 0078971-A 7 28-DEC-2000;
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1 (Dases 1 to 104/4)

Lawn, R.M., Wade, D. and Garvin, M.

Regulation with binding cassette transporter protein abcl

Patent: WO 0078972-A 9 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
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2304 c 2415 q 2844
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. Is the number of results predicted by clance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 2, Appli	Sequence 101, App	Sequence 101, App	Sequence 5, Appli	Sequence 26, App.	Sequence 25, Appl	<	Sequence 10, Appl	sequence 92, Appl	Sequence 93, Appl	Sequence 94, Appl	Sequence 95, Appl	Sequence 96, Appl	97.		. '66	Sequence 100, App	Sequence 101, App
SUMMARTES	ID	US-09-984-827-4	0 US-09-846-456-2	US-09-924-346-:01	US-09-992-600A-101	0 US-09-846-456-5	US-09-584-827-26	US-09-984-827-25	US-09-984-827-1	0 US-09-846-456-10	US-09-984-827-92	US-09-984-827-93	US-09-984-827-94	US-09-984-827-95	US-09-984-827-96	US-09-984-827-47	US-09-984-827-98	US-09-984-827-99	US-09-984-827-100	US-09-984-827-101
	ouery Match Length DB	357 9	357 10	1062 9	1062 9	159 1	159 9	158 9	9741 9	9741 1	9870 9	9870 9	9870 9	9870 9	9870 9	9870 9	9870 9	9870 9	9870 9	9870 9
gá.	Query Match 1	100.0	100.0	57.1	57.1	44.5	44.1	41.2	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8	40.8
	Score	357	357	203.8	203.8	159	157.4	147	145.8	145.8	145.8	145.8	145.8	145.8	145.8	145.8	145.8	145.8	145.8	145.8
	Result. No.	-	?	m	4	S	9	7	æ	6	10	11	12	13	14	15	16	17	18	19

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Length 357; Indels

Score 357; DB 9; I Pred. No. 1.6e-108;

Query Match
Best Local Similarity 100.0%;
Matches 357; Conservative 0;

; ORGANISM: Homo sapiens US-09-984-827-4

TYPE: DNA

0; Mismatches

61 ATAACTGAFGCFGTTTCCCCTCCTCCTTATCTTTCAGTTAATGACCAGGGGGGT 120

61 ATAACTGATGGCTGTTTCCCCTCCTGCTTTATCTTTCAGTTAATGACCACGGCGGT 120

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121 CCCTGCTGTCAGCTCTGGCCGCTGCCTTCCAGGGCTCCCGAGCCACACGCTGGGCGTGCT 180

92

-102 Sequence 102,	827-103 Sequence 103, App	27-104 Sequence 104,	27-105 Sequence 105,	27-106 Sequence 106,	107,	827-108 Sequence 108,	827-109 Sequence 109,	827-110 Sequence 110,	27-111 Sequence 111,	27-112 Sequence 112,	27-113 Sequence 113,	27-114 Sequence 114,	27-115 Sequence 115,	-116 Sequence 115,	-117 Sequence 117,	827-118 Sequence 118,	119 Sequence 119,	.20 Sequence 120,	.21 Sequence 121,	827-122 Sequence 122,	827-123 Sequence 123,	.24 Sequence 124,	-125 Sequence 125,	-126 Sequence 126,	
US-09-984-827	US-09-984-	08-984-8	08-08-984	08-09-884-	•	-09-984-	•	- <b>18</b> -60-SN	US-08-684-	US-08-984-8	-\$86-60-Sn	08-09-984-	US-09-984-	US-09-984-827	US-09-984-827-		OS-09-984-	US-09-984-827-	US-09-984-827-1	- 186-60-Sn	-09-984-	US-09-984-827-1	US-09-984-827	US-09-984-827	
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TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABIAL SENE, THEIR USES, TITLE OF INVENTION: DEFECTION METHODS AND KITS THEREFOR

FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: FR 00/14037 PRIOR FILING DATE: 2000-10-31 NUMBER OF SEQ 10 NOS: 161 SOFTWARE: PALENLIN VET. 2.1 SEQ 1D NO 4 LENGTH: 357

APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE APPLICANT: ARNOULD: REGULGME, ISABELLE APPLICANT: DUVERGER, NICOLAS APPLICANT: CAMBIEN, FRANCOIS

Sequence 4, Application US/09984827 Publication No. US20030056234Al GENERAL INFORMATION:

APPLICANT: DENEFLE, PATRICE

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99 GITAATGACCAGCTACGGGCGTCCTGCTGTCAGCTCTGGCCGCTGCCTTCCAGGGCTCC 158
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                                                                                                                                                                                                      APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.022.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
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Publication No. USS0030027161A1
CENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tacaka, Hiroaki
TILLE OF INVENTON: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91, USA, DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Score 203.8; DB 9; Length 184.8%; Pred. No. 1.8e-57;
tive 0; Mismatches 42; Indels
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PRIOR FILING DAIE: 2001:07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001:06-15
PRIOR FILING DATE: 2001:06-15
PRIOR FILING DATE: 2001:06-15
PRIOR FILING DATE: 2001:06-15
SOFTWARE: 1944Ent.
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                                Sequence 101. Application US/09924340 Publication No. US20030027248Al GENERAL INFORMATION:
                                                                                                                                                                      APPLICANT: Bejanin, Stephane
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NAME/KEY: polyA_signal
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polyA_site
1047...1052
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US-09-992-600A-101
US-09-924-340-101
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NAME/KEY:
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LOCATION:
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APPLICANT: Duverger, Nicolas
APPLICANT: Brewer, Bryan
APPLICANT: Remairey, Alan
APPLICANT: Fojo, Silvia
TITHE OF INVENTION: Regulatory Nucleic Acid for the ARC1 Gene. Molecules Modifying 10
TITHE OF INVENTION: Activity and Therapeutic Uses
FILE REFERENCE: 3806.0505
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Patent No. US20020146792Al
GENERAL INFORMATION:
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APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
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Best Local Similarity 106.0
Matches 357; Conservative
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URGANISM: Homo sapiens
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APPLICANI: F030, Silvia
TITLE OF INVENTION: Regulatory Nucleic Acid for the ABC1 Gene, Molecules Modif
TITLE OF INVENTION: Activity and Therapeutic Uses
TITLE REFERENCE: 3466,0505
CURRENT APPLICATION NUMBER: US/09/846,456
CURRENT APPLICATION NUMBER: US 60/201,280
PRIOR APPLICATION NUMBER: US 60/201,280
PRIOR FILING DATE: 2000:05-02
NUMBER OF SEO ID NOS: 20
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APPLICANT: ARNOLD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TILLE OF INVENTION: PROGRAMMEND SEQUENCES OF THE HUMAN ABCA, GENE, THEIR USES,
TILLE OF INVENTION: PROGRAMMEND SAND KITS THEREFOR
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100.0%; Pred. No. 6e-43;
Live 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: 05/09/984,827
CURRENT FILING DATE: 2052-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
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Publication No. US2003005624481
GENERAL INFORMATION:
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Conservative 0
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SOFTWARE: Patentin Ver. 2.1
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Matches 159; Conserv
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US-09-984-827:26
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Live 0; Mismatches 42; Indels Design
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PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IBU1/01715
PRIOR APPLICATION NUMBER: QS 0/305,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR PLILING DATE: 2001-06-29
PRIOR PLILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/296,698
PRIOR PPLICATION NUMBER: US 60/294,574
PRIOR PPLICATION NUMBER: US 60/294,574
PRIOR PPLICATION NUMBER: US 60/294,574
PRIOR PPLILING DATE: 2001-06-15
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Patent No. US20020146792A1
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Naudin, Laurent
Denefle, Patrice
Duverger, Nicolas
Brewer, Bryan
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APPLICANT: Prades, Catherine
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LOCATION: 1023..1028
FEATORE:
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ORGANISM: Homo sapiens
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; UxYATIGN: 1047..1062
US-09-992-600A-101
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Matches 240; Conserv
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LOCATION: 640..1062
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LOCATION: 154..639
FEATURE:
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SEQ ID NO 101
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SOMATION: 1..153
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Regulatory Nucleic Acid for the ABCI Gene, Molecules Modify TITLE OF INVENTION: Activity and Therapeutic Uses FILE REFERENCE: 8466,6505 CURRENT APPLICATION NUMBER: US/09/846,456 CURRENT FILING DATE: 2001 05-02 PRIOR APPLICATION NUMBER: US 60/201,280 PRIOR APPLICATION OF 05-02 PRIOR APPLICATION OF 05-02 PRIOR APPLICATION OF 05-02 PRIOR APPLICATION DATE: 2000 05-02 PRIOR FILING DATE: 2000 05-03 PRIOR PRIOR FILING DATE: 2000 05-03 PRIOR PRIOR FILING DATE: 2000 05-03 PRIOR FILING DATE: 2000 05-03 PRIOR PRIOR FILING DATE: 2000 05-03 PRIOR PRIOR FILING DATE: 2000 05-03 PRIOR PRIO
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TESTION STATEMENT OF THE TERRITOR STATEMENT OF THE STATEMEN
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CTHER INFORMATION: "n" is closen from 9, a, t and
US-09-846-456-10
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Patent No. US20020146792Ai
GENERAL INFORMATION:
                                                                                                                                    APPLICANT: Prades, Catherine APPLICANT: Lemoine, Cendrine APPLICANT: Naudin, Laurent APPLICANT: Denetie, Patrice APPLICANT: Brewer, Nicolas APPLICANT: Remaley, Alan APPLICANT: Femaley, Alan APPLICANT: Fond, Silvia
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US:09-846-456-10
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Publication No. US20030056234A1

General incommenture. Patrice

APPLICANT: Denrele. Patrice

APPLICANT: DENRELE. PATRICE

APPLICANT: DENRELE. SEGUIONE. ISAHELLE

APPLICANT: GENER MONTUS. MARIE-FRANCCISE

APPLICANT: CARBIEN. PRANCOLS

APPLICANT: CARBIEN. PRANCOLS

APPLICANT: CARBIEN. PRANCOLS

TITLE OF INVENTION: DELECTION METHODS OF THE BUKAN ANY, GENE, THEIR USES. AND

TITLE OF INVENTION: DELECTION METHODS

FILE REFERENCE: 03806, 0522-00000

CURRENT FILING DATE: 2002-04-01

PRIOR FILING DATE: 2000-12-11

PRIOR FILING DATE: 2000-12-11

PRIOR FILING DATE: 2000-12-11

PRIOR APPLICATION NUMBER: FR 20/140-7

WINHER APPLICATION NUMBER: FR 20/140-7

WINHER CATCH OF MOSE 16.
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APPLICANT: ARMOULD REGICENE, ISABELLE
APPLICANT: ARMOULD REGICENE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TUTLE OP INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARGA: GENE, THEIR USES, AND
FILE REFERENCE: 03806,0522-00000
CURRENT PEPPLICATION NUMBER: US/09/984,827
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-10-31
NUMBER: PARCOIT STATE SOURCES SCHUKES: 161
NUMBER: PARCOIT STATE SOURCES SCHUKES: PARCOIT STATE SCHUKES: PARCOIT SCHUKES: PARCOIT STATE SCHUKES: PARCOIT SCHUKES: PARC
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121 CTGCTGTGGAAGACCTCACTTTCAGAAGACACAAAGA 159
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Publication No. US20030056234A1
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
SEG 10 NO 1
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Matches 158; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: DENEFLE, PATRICE
APPLICANT: DENEFLE, PATRICE
APPLICANT: ARMOUTS, MARIE-FRANCOISE
APPLICANT: ARMOUTS-REGUIGNE, ISABELLE
APPLICANT: ARMOUTS-REGUIGNE, ISABELLE
APPLICANT: CAMBIEN: FRANCOIS
TITLE OF INVENTION: PULYMORPHIC SEQUENCES OF THE HUMAN ABCALGENE, THEIR USES, TITLE OF INVENTION: DELECTION METHODS AND KITS THEREFOR FILE REFERENCE: 03805, 0522-00000
FILE REFERENCE: 03805, 0522-00000
FULLE REFERENCE: 03805, 0522-00000
FULLE REPERENCE: 03805, 0522-00000
FRIOR APPLICATION NUMBER: 60/254, 108
PRIOR APPLICATION NUMBER: 60/254, 108
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR APPLICATION NUMBER: FR 00/14037
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                                                                                                                                                                                                                                                                                                                                                                                                                                         40.8%; Score 145.8; DB 9; Length 80.9%; Pred. No. 8.3e-38; Store 0; Mismatches 42; Indels
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Pred. No. 8.3e-38;
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CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Vel. 2.1
SEQ ID NO 93
LENGTH: 9870
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80.9%;
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; OTHER INFORMATION: a, L. C v
US-09-984-827-93
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Best Local Similarity 80.93
Matches 182: Conservative
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Best Local Similarity 80.9
Matches 182; Conservative
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SOFTWARE: Patentin Ver. 2
                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
LOCATION: (7138)
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                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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APPLICANT: DENEFLE, PATRICE
APPLICANT: DENEFLE, PATRICE
APPLICANT: ARNOLLD-REGUIGNE, ISBELLE
APPLICANT: ARNOLLD-REGUIGNE, ISBELLE
APPLICANT: DUVERGER, MICOLAS
APPLICANT: DUVERGER, MICOLAS
APPLICANT: DUVERGER, MICOLAS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HEMAN ABVALENE; FREIR USES, AND
TITLE OF INVENTION: DETECTION MITHODS AND KIIS THEREFOR
FILLE REPERENCE: 03806.052-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT APPLICATION NUMBER: 00/204-01
PRIOR APPLICATION NUMBER: ER 00/14037
PRIOR APPLICATION NUMBER: ER 00/14037
PRIOR FILLING DATE: 2000-10-31
NUMBER: OF SEO ID NOS: 161
SETUM FOR FILLING DATE: 2000-10-31
NUMBER: OF SEO ID NOS: 161
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FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: 05/09/844.827
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        209 TIGCIGCTGCTGGAAGAACCTCACTTTCAGAAGAAGAAAAATAIGTCAGCTGCTGCTGGAA 248
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40.8%; Score 145.3; PB 9; Locath 9
Best Local Similarity 80.9%; Pred. No. 8.3e-38;
Matches 182; Conservative 0; Mismatches 42; Ind-19
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APPLICANT: ROSIER-MONTOS, MARIE-FRANCOISE
APPLICANT: ANNOUD-REGUIGNE, ISABELLE
APPLICANT: DIVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
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Sequence 92. Application US/09984827
Publicatios No. US20030056234Al
GENERAL INFORMATION:
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US-09-984-827-92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (7138)
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GENERAL INFORMATION:
APPLICANT: DENERLE, PATRICE
APPLICANT: ROSIER-MONIOS. MARIE-FRANCOISE
APPLICANT: ANNOUND: MARIE-FRANCOISE
APPLICANT: ANNOUND: MARIE-FRANCOISE
APPLICANT: DUVERCER, NICCLAS
APPLICANT: DUVERCER, NICCLAS
APPLICANT: CAMBIEN, FRANCOIS
ITILE OF INVENTION: ONLY OF ANNOUNCES OF THE HUMAN ABCALGENE, HEIR USES,
ITILE OF INVENTION: ONLY ONLY ONLY ONLY
CORRENT APPLICATION NUMBER: 05/09/984,827
CORRENT APPLICATION NUMBER: 05/09/984,827
CORRENT APPLICATION NUMBER: 60/254,108
PRIOR PILING DATE: 2000 i2 11
PRIOR FILING DATE: 2000 i2 11
PRIOR PILING DATE: 2000 i2 11
SOFTWARE OF SEO 1D MUSE: 61
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APPLICANT: DENERTE: PATRICE
APPLICANT: ROSIER-MONTOS, MARIE-FRANCOISE
APPLICANT: OUVERGER, NICTARS
APPLICANT: CARRIEN, FRANCOIS
APPLICANT: CARRIEN, FRANCOIS
APPLICANT: CARRIEN, FRANCOIS
APPLICANT: CARRIEN, FRANCOIS
ITILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
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80.9%; Pred. No. 8.3e-38;
Live 0; Mismatches 42;
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ 1D N'S: 163
SOFTWARE: Patestli Vet. 2.1
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Publication No. US/09/3056294A1
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ORGANISM: ROBO, SAPORTA
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LENGTH: 9870
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LENGTH: 987
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APPLICANT AND CONCERNORS, MAKEE-FRANCUISE
APPLICANT AND COLOR ISOLOGICE, ISABELLE
APPLICANT AND COLOR MOSI AND MOSI AND TITLE OF INVENTION POLYMORPHIC SEQUENTES OF THE HOMAN AND THERE AS AND TITLE OF INVENTION POLYMORPHIC SEQUENTES OF THE HOMAN AND THE SECOND OF THE OF INVENTION OF DETECTION WETHOUS AND KITS THEREPORE
FILE OF INVENTION OF DATE: 2002-904,827
CURRENT APPLICATION NUMBER: 05/09/984,827
CURRENT APPLICATION NUMBER: 05/09/984,827
CURRENT APPLICATION NUMBER: 60/254,108
PRICHE APPLICATION NUMBER: 60/254,108
PRICHE APPLICATION NUMBER: 60/14047
PRICHE APPLICATION NUMBER: R 60/14047
PRICHE PRICHE FILING DATE: 2000-10-31
NUMBER OF SEC 1D NOS: 161
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: Publication No. US20030056234A1
: GENERAL INFORMATION:
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Publication No. US20030056234A1
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ą	781	GATGAAACAGAGGCAGAAAGACTTTACGTAAATTGCTCATCATGTGGTTGTFAAGTTTGA	84()
ž g	641 841	COCCAAAACCCAATTATTGACCAAGGTTATTCTTTCACTGAGGGGAGGGGGTCGGTC	906 006
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<b>☆</b> 광	961	ATTITCIGACACGGAGICIIGCICIUI CACCAGUGGCUGGAGIGGAGIGG 	
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<u> </u>	1061 1081	GATAACAGGCGCCGCCACCACCACCTGGCTAA;TTTTGTATTTTTAAAAA3A71GGSTF 	
à é	1141	TCATCATGTTGGCCAGGTTGGTTTCGAACTCCTGACCTGAGGTGACGTGCCCACCTTGUC 	0 0
40 40		CICCCAAAGIGCIGGGATTACAGGCATGAGCCACIGCUCCCAGCICAGATCCAICCCITT	
88 a	1251 1261	CTAAGGODAAACAGTCCATGGTGCAAAGGGGCCATGCCACCAGAGTTATGAGTACCTGG 	C1 : Y
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չ Տ	1501	TOCAGGTGGTGGGAGTTCTGGAATATGATGGGGGTTGGAGGGGGGGAAAGAGAAAGTAGGTTGGTTTGAATGATG	9 9
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27 26	1621 1621	AAATGTGAATGTGCCCTTCAAGGTGGCTACAAAGGTATCT : LOTCAAGGTAGGAAGCTT 	1680 1680
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₹ g	1741	CTTCTATGAATCCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTLGAGGGGGGGTTT 	1800 1800
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ž a	1861	CTTGCCTTTTTTTTGCCCCTCCAGECT HTMLHTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1920 1920

Oy	1921	AGITTIGCTCCCCIACAGCCAAAGGCAAACAGAGAGTTGGAGGTCTGGAGTGGATACAT 1980	0.0
qa	1921	TTTTGCTCCCCTACACAAAGGCAAACAGAAGTTGGAGGTCTGGAGTGGCTACAT	30
ò	1981	AATITTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAA 2040	0
Oto		ITTACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAA	0.1
QY		FATCACAGGAGGCTGATCAATATAATG	00
a	2041	DOTGROTH: TEATCACAGGGAGGCTGATCAATATAATGAAATTAAAAGGGGGCTGGTC	00
ογ	2101	AATGFTCFGTGTTTTTGTTTGTTTTGTTTGTTTGTTTTTTTT	0.0
qq		ATATTGITCTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTT	0
ολ	2161	CTTCCTCTCAATTTATGAAGAGAGAGTAAGATGCTCCTCGGGTCCTCTGAGGA	0
g		CCCCCCAATTTATGAAGAAGCAGTAAGATGTTCCTCTCTCT	0
ģ	2221	TGGGGGGCTCAGGCTGGGAATCTCCCAAGGCAGTAGGTCGCCTATCAAAAATCAAAGTC	0
ąc		DIGGGGGGCCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTC	0
Oy	2281	GTTTGTGGGGGAAAACAAAAGCAGCCCATTACCAGAGGACTGTCGGCCTTCCCCT	0
qq	2281	STITIGLGGGGGAAAACAAAGCAGCCCATTACCCAGAGACTGTCGGCTTCCCCT	0
δò	2341	CCCAGCCTAGGCCTTTGAAAGGAAACAAAAAGACAAAAGACAAAATGATTGGCGTCCTGA	00
Op.	2341	ACCCAGCCTAGCCTTTGAAGGAACAAAAGACAAAGACAAATTGGCGTCCTGA	0
ć	2401	GALTCAGCCTAGAGCTCTCTCCCCCAATCCCTCCCTCCGGCTGAGGAACTAAC	0
qu		SAGATTCACCCTAGAGGTCTCTCTCCCCCAATCCCTCCCTC	0.0
ς	2461	AACCAGGATTAAGAGGAAGCAAATTCCACTGGTGCCCTT	0
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δλ	2521	SUCARCOTEGACTACACACTCTCCCCCCCCCCCCCCCCCCCCCCCCC	30
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5	2581	NGGCGGGGGGGGGGGGGGGAAGGGGACGCAAACGCGGGGACCCTAAGACA	0,
q	2581	STOTTAGGGGGGGGGGGGGGGGGAAGGGGACGCAAACGGGGACCCTAAGACA	01
ç	2641	CIGIACCTCCACCCCCACCCCACCCACCCACCCCCAAAGTGG	00
đ		CTGCTGTACCCTCCCCCCCCCCCCCCCCCCCCCCCCCCC	00
QY	2701	STGGGGGGGTGAACGTCGCCCGTTTAAGGGCGGGCCCCGGGCTCCACCTGCTTCTGC	0.0
ପୁମ	2701	SG1GGGGGGGTGAAGGTCGCCCGTTTAAGGGGGGGGGCCCCGGCTCCACGTGTTTCTGC	0
Oy	2761	TGACTGAACTACATAAACAGAGGCCGGGAAGGGGGCGGGGGGGG	0
qa	2761	SAGTGACTURACTARACAGAGGCCGGGAAGGGGGGGGGGGGGGGGGGGG	0
ογ	2821	CTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCC	0
an	2821	TITGACCGALAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGGAACTAGTCC	0
ολ	2881	TTGCGAGCGAGAGTGAGTGGGCCGGGACCCGCAGAGCCGAGC	0
વૃદ્ધ	2881	GCAAAAACCCCGTAATTGCGAGCGAGAGTGAGTGGGGCCGGGACCCGCAGAGCCGAGG	0
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qe	2941	CCTICICICACOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	0

300 CGGTTCTCAGGGGCTTTGTTTTTTCTCCGGTTTTTTTCCCTTTTTTTCTCCGTTTTTT

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                    ACCCTGTCTCTACAAAAAAAAAAAATACAAAAATTAGATGGGTGTGGTGGCATGCACCTGTGGT
                                                                                                CTGAGCCATGATTGGATCACTGCACTCCAGCCTGGGTAGACAGAGCAAGACCTGTCTCA
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78232. 125269,125285. 12544,125754. 125870,

78079. 130276. 131023. 131028. 131749. 131925.

78268. 138381,140179. 140350,141340. 141471,

78268. 13881,140179. 140350,141340. 141471,

784777. 142919,143123. 146859,148527. 148575,

78481. 145513,146657. 146859,148527. 148575,

78481. 151536,15568. 156757,158278. 152202,

785682. 155714, 160842, 15677,158278. 158491,

786815. 156959,16681. 1565681,577,158278. 167844,

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786828. 174488. 174889,174961. 175095,176039. 1771942.
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Olu,Y., Cavelier,L., Chiu,S., Rubin,E. and Cheng,J.-F.
Direct Submission
Submitted (13-J8L-2000) Genome Science Department, Lawrence
Berkeley, National Laboratory, 1 Cyclotron Rd, MS 84-171, Berkeley,
CA 94720, USA
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1 (Dases 1 to 201144)

Qiu.Y. (ZevelerL., Chlu, S., Yang, X., Rubin, E. and Cheng, J.F. Human and mouse ABCAl comparative sequencing and transgenesis studies revealing novel regulatory sequences

Cenomics 73 (1), 66-76 (2001)
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/db_xref="taxon:9606"
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/gene="ABCA1"
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Santamarina-Folo,S., Peterson,K., Knapper,C., Oiu,Y., Freeman,L., Cheng,J.F., Osoilo,J., Remaley,A., Yang,X.P., Haudenschild,C.,
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Prades.C., Chimini.G., Blackmon.E., Francois.T., Duverger.N.,
Rubin,E.M., Rosier.M., Denefle,P., Fredrickson.D.S. and Brewer.H.B.
                                                                                                       Complete genomic sequence of the human AHCA1 gene: analysis of the human and mouse ATP-binding cassette A promoter Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2003)
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Sandamina-Folo,S., Peterson,K.M., Knapper,C.L., Fiveman.L.A.
Remaley,A.T., Yang,X.-P., Haudenschild,C.C., Blackwon,E.E.,
Francois,T.L. and Brewer,H.B. Jr.
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Submitted (08-UNN-2000) Molecular Disease Branch, National
Institutes of Heath, National Heart, Lung and Blood Institute.
Hethesda, MD 20892, USA
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MDPKARKFLWNCALSVVKEGRSYVLTSHSMEECEALCTRMAJMYNGRFRCLGSVQHLK
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Direct Submission

Notice 1.

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The true right end of clone RPI1-12187 is at 96777 in this sequence. The true left end of clone RPI1-122710 is at 25980 in this sequence. The true right end of clone RPI1-31260 is at 2660 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL359182 96717 bp DNA linear FRI 11-JAN-2002 Human DNA sequence from clone RPI1-21787 on chromoscame 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
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Catarriini; Hominidae; Homo,
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RPI1-217B7 is from the library RPCI-il.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/d_elegans/wormpep_This_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $160
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                                  CGACCCTTCTCTCCCGGGCTGCGGCAGGCCAGGCGGAGCTGCGCGCACCAACAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3181 AAGTGCTCGGTTTCGGGGACTTTGATCCGGAGCCCCACATCCCCACCACTT 3231
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Mammalia, Eutheria, Primates,
1 (bases 1 to 96717)
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                                                                                                                                                                                                                                                                                     /note-*Sequence from reads from a short insert library derived from a single puc clone. Restriction digest data confirm the assembly.*
27673 a 21138 c 20380 g 27526 t
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                                                                                                                                          Institutes of Heath, National Heart, Lung and Blood
Institute, Bethesda, MD 20892, USA."
84245, 84273
/note-"Sequence from overlapping clone RPI1-122F10
ACO26643, Assembly confirmed by restriction digest."
92050, 92163
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/note-"Sequence from AF275948 sequenced by National
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99.7%; Pred. No. 0;

    95/1/
/organism="Homo sapiens"
/db_xref="taxon:9606"

                                                                                                 /clone_lib-"RPC1-11.1"
            Location/Qualifiers
                                                                    /chromosome="9"
/clone="RP11.21787"
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this sequence.
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Eukaryota, Metazoa, Chordata, Cranidta, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Cleu, S.M. Compositions and methods for modulating hid cholesterol and triglyceride and methods for modulating hid cholesterol and patent. Wo 0115676-A 1 08-MAR 2001, University of British Columbia (CA); Nerum Hearlies Inc. (C
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                                                   FGGGC1TGAGCCGTGGCCTGGAGATCCTGTTGTAGCATCGAGGGGGTTLGTGGAGG
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Pred, No. 0;
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/db_xref-"taxon:9606"
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Bald≆in,J., Barna,N., Beckerly,R., Boguslavkly,L., Boukhgalter,B.,
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Homo sapiers clone RP11-1M10, WORKING DRAFT SEQUENCE, 39 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                        TCTATGCGTCTGTCTGTGAGTGTTGATAGAACCACTGATGTGAGTACCTGGGCTTGAGCCG
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                                                        ATAACAGGGGGGGGGCACCACATCTGCATTTTTTTAGTAAAGACTGGGTTT
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1 (Dases I to 17504)
Bhirten, B., Linton, L., Nusbaum, C. and
Homo sapiens, clone RPII-1M10
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68437: contig of 4676 bp in length
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76888: contig of 5330 bp in length
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Hrown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donclan, L., Doyle, M., Perreira, P., Fitzhugh, M., Forrest, C., Funke, R., Gaqe, D., Calaqan, J., Gardyna, S., Grant, G., Hagos, B., Heatord, A., Hortch, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Kararas, A., Klein, J., Hewland, J.C., Loeke, K., Macdonald, P., Maratis, A., Klein, J., Horrow, J., Naylor, J., Norman, C.H., O'Connor, I., C'Inonnell, F., Peterson, K., Pollara, V., Riley, R., Koy, A., Santos, K., Severy, P., Stangerihomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (21-007-1999) Whitehead institute/MIT Fente: for Genome Submitted (21-007-1999) Whitehead institute/MIT Fente: JSA on Apr 22, 2000 this sequence version replaced quin454034.
All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.cdu/HM/HepcatMasKer html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
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9687 9786: gap of 100 bp
12294 12353: gap of 150 bp
12294 12353: gap of 150 bp
12354 15528: contig of 2875 bp in length
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contig of 1872 bp in length
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28184: contig of 2377 bp in length
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ARIZOMO2381 1167 bp DNA linear PRI 29-JUN-2000 Homo sapiens ATP binding cassette transporter 1 (ABCA1) gene, promoter and exon 1.
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Bukaryota: Metazoa, Chordata; Craniata; Vertebrata: Euteleostoml;

Mammalia: Eutheria; Primates; Catarrhini; Hominidae: Homo.

1 (bases 1 to 1167)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,

Andizerta, B.E., Fielding, C.J. and Kane, J.P.

Analysis of hARGI gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

Blochem Blophys. Res. Commun. 271 (2000) In press

2 (bases 224 to 1167)

Pullinger, C.R., Hakamata, H., Duchateau, P.N., Eng, C.,

Abouizerat, B.E., Fielding, C.J. and Kane, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20 APR-2000) Cardiovascular Research Institute, University of California, San Francisco, 505 Parnassus Avenue, Francisco, CA 94143-0130, USA (bases 1 to 1167)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata: Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. I hases ito 1167)
Porsch-Ozcurumez,M., Langmann,T., Heimerl,S., Borsukova,H., Kaminski,W.E., Drobnik,W., Honer,C., Schumacher,C. and Schmitz,G. The zinc inger protein 202 (ZNF202) is a transgriptional repressor of AIP binding cassette transporter Al (ABCA1) and ABCG1 gene expression and a modulator of cellular libid efflux
J. Biol. Chem. 276 (15), 12427-12433 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (05-JAN-2000) Porsch-Oezcueruemez M.K., Institute for
Clinical Chemistry. University of Regensburg,
FRanz-Josef-Strauss-Allee 11, 93042 Regensburg, GERMANY
Location/Qualifiers
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                                                                      1910 GTGAGTGGGGGGGCCCCCCCAGAGCCGACCCGACCCTTCTCTCCCCGGGCTGCGGCGAGGG
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| 315 c 327 g 247 t
                                                                                                                                                                                                                                                                                                                                                                                                                             HSA252201 1167 bp DNA linear PRI : Homo sapiens partial ABC-1 gene for ATP-binding cassette transporter-1, 5'UTR and promoter region.
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/db_xref-"taxon:9606"
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/cell_type="leukocyte"
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Porsch-Oezcueruemez,M.K.
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        Vertebrata; Euteleostomi;
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      Craniata; Ve
Catarrhini;
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Entwaryota: Metazoa: Chordata; Craniat
Mammalia: Butheria: Primates; Catarrh
1 (bases 1 to 1643)
Lawn, R.M.: Made, D. and Garvin, M.
Regulation with binding cassette tran
Patent: WO 001897-2 A 3 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
Location/Qualifiers
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                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
| 413 c 457 a ^^^
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AC021246
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutenta, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1643)
Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.
Atp binding cassette transporter protein abel polypeptides patent: Wo 0078971-A 3 28 DEC-2000;
CV THERAPEUTICS, INC. (US)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidue, Homo,
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Pred. No. 9.8e-259;
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Strenger in the control of the c
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* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               • NOTE: This record contains 73 individual
• sequencing reads that have not been assembled into
• contigs. Runs of N are used to separate the reads
• and the order in which they appear is completely
• arbitrary. Low pass sequence sampling is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 841 bp in length of 100 bp contig of 851 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sgap of 100 bp 5640; contig of 844 bp in length
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12403 13280: contiq of 878 bp in length
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0: gap of
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3845: gap of
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* 13281 * 13381	24	45.0	529	512 522	707	304	2 2	19110	986	955	102	961	283	378	988	183	577	562	757	767	9 C 0 C 0 C	946	459	055	14:	236	331	341	4 .6	520	615	712	722	9 20	903 913	000	960	106	201	282	377	387	4 / 5 4 8 5	572	382 664	674	် ၁

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60984 61083; gap of 100 bp 61084 61085; contig of 822 bp in length 61084 62866; contig of 822 bp in length 62867 62866; contig of 831 bp in length 62867 62867; contig of 861 bp in length 63828 63427; gap of 100 bp 63928 64783; contig of 856 bp in length 63928 64884 6883; contig of 857 bp in length 65741 65846; contig of 857 bp in length 65841; gap of 100 bp 6688 66784; gap of 100 bp 66785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.29 53.428: qap ol 100 bp 53.29 53.428: qap ol 100 bp 53.429 54.268: contig ol 840 bp in length 54.269 54.368: qap ol 100 bp 55.229: contig ol 861 bp in length 55.230 55.249: qap ol 100 bp 55.30 55.29: qap ol 100 bp 55.30 55.329: qap ol 100 bp 56.39 56.29: qap ol 100 bp 56.298 57.263: contig ol 866 bp in length 57.164 57.263: qap ol 100 bp 57.264 58.130: contig ol 867 bp in length 58.31: 59.082: contig ol 85.2 bp in length 59.83: qap ol 100 bp 
                                                                                                                                                                                                                                     50441 50540: qap of 100 bp 50541 51404: contig of 864 bp in length 51404: gap of 100 bp 52172: contig of 868 bp in length 52173 52472: qap of 100 bp 52473 53428: contig of 856 bp in length
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                                72 48651; gap of 100 bp

72 49485; contig of 834 bp in

86 49585; gap of 100 bp

65 50440; contig of 855 bp in

11 50540; gap of 100 bp

11 51404; contig of 864 bp in
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60983: contig of 863 bp
contig of 852 bp
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48551:
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Best Local Similarity 99,7%
Matches 398; Conservative
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56194 5629;
57164 57263;
57164 57263;
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; 0 100 bp f 1994 bp in length

100 bp of 1270 bp f

in length

in length

in length

in length in length in length

in length in length

ACCESSION VERSION KEYWORDS SOURCE KEFERENCE AUTHORS

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17 103116: 93p of 100 bp
18 109178: contig of 6062 bp in length
19 109278: contig of 6062 bp in length
19 103279: gap of 100 bp
18 117307: contig of 8029 bp in length
18 11407: gap of 100 bp
18 124079: contig of 6672 bp in length
18 124179: gap of 100 bp
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138059: contig of 6678 bp in length
8159: gap of 100 bp
145491: contig of 7332 bp in length
5591: gap of 100 bp
157391: contig of 11800 bp in length
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175064: contig of 17573 bp in length.
                                                                                                                                                                                                          9786: gap of 100 bp
12253: contig of 2467 bp in length
1253; gap of 100 bp
15228: contig of 2875 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99: gap of 100 bp 97901: contig of 4302 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                  oof 100 bp
contig of 2831 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                      p of 100 bp contig of 2356 bp in length
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88220: contig of 6007 bp
88320: gap of 100 bp
93499: contig of 5179 bp
                                                                                                                                                   of 100 bp contig of 1707 bp
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contig of 4417 bp
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28284: gap of
31338: cont
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Baldwin.J., Barna.N., Beckerly.R., Boquslavkiy.L., Houkhqalter.B.,
Brown,A. Castla.A. Colangelo.M., Collins.S., "Callymore.A.,
Cooke.P., Darellano.K., Dewar.K., Domino.M., Dorlelan.L., Doyle.M.,
Eerreira,P., FitzHugh,W., Forrest,C., Funke,P., Gage.L.,
Galagan.J., Gardyna.S., Grant.G., Hands.B., Warquis.N.,
Howland,J.C., Johnson.R., Jones.C., Kann.L., Karatas.A., Klein,J.,
Lehocrky.J., Lleu.C., Locke.K., McChaughin.J., Marquis.N.,
McTow,J., Naylor.J., Norman.K., McLaughin.J., McHaill.P.,
Peterson,K., Pollara.V., Rifey.R., Koy.A., Sant.S.R., Severy.P.,
Stange-Thomann.N., Stojanovic.N., Subramanian.A., Talamas.J.,
Trestaye.S., Tirrell.A., Vassiliev.H., Wo.A., Wheeler.J., Wu.X.,
Wyman.D., Ye.W.J., Zimmer.A. and Zody,M.
No Direct Submission
No Street. Cambridge. MA 02141, USA
On Apr. 22, 2000 this Sequence version replaced qiick454033.
All repeats were identified using RepeatMasker:
                                                                                                                                                      HTG 22-APR-2000
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 175064)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is
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insert size: 171264; sum-of: contius
Quality coverage: 2-9 in Q20 bases; agarose-fp
Quality coverage: 3-2 in Q20 bases; sum-of-contigs
                                                                                                                                                      AC012230 175064 bp DNA Linear H1
Homo sapiens clone RP11-1M10, WORKING DRAFT SEQUENTE.
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http://ftp.genome.washington.edu/kM/kepeatMask++1.html
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------ Project Information
Center project name: L25i9
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2635 2734; gap of 100 bp
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Consensus quality: 160940 bases at least G20
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Sequencing vector: M13; M778ib: 100% of re
Chemistry: Dye-terminator Bid Dye: 100% of
Assembly program: Pitrap; version 0:9667il
Consensus quality: 11757l bases at least C
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               Db 41727 CTCCCCAAGCCTTGTCAAGCCGTACCAGAAAGAGGCCA 41765
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Web site: http://www-seq.wi.mit.edu
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Homo sapiens, clone RP11-1M10
Unpublished
                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT.
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AC012230.3 GI:7637254
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                                                                                             RESULT 13
AC012230/c
                                                                                                                                                                                 DEFINITION
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AUTHORS
TITLE
JOURNAL
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JOURNAL COMMENT

in length

in length: in length 100 bp f 5179 bp in length

in length in length

100 bp f 5125 bp

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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:acnomics/hii.co.)p, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO Luman cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5-6-3-64 one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center Ctc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
                                                                                                                                                                                                                                                                                                                                                                                                       PRI 01-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai, I., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nayai, K., Sugano, S., Takahashi-Fujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y., and Oshima, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryolu; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2896 AATTGCGAGGGAGGTGAGTGGGGCCGGGACCCGAGAGCCGAGCCGACCCTTCTCTCCC 2955
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                                                       215 AAATCATGCTAGGAAAGATAACACCTTTTAATAACACTGTCTGCTTTTATAACATCATTC
                                                                                                                                                                                                   335 AGAATATACATGTTCTCTCCATTTTAAAGATGAAGAACAGGCCGGGCACAATGGGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                   AK022254 Innear PRI 0 homo sapiens cDNA FLJ12192 fis, clone MAMMA1000851. AK022254 AK022254 I G1:1043.612 olido capping: fis (full insert sequence). Homo sapiens Mammary gland cDNA to mRNA, clone_lib:MAMMA1000851.
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/clone_lib="MAMMA1"
/note="cloning vector: pME18SFL3"
1 489 c 586 g 384 t
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/db_xref="taxon:9606"
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Best Local Similarity 100.C
Matches 336; Conservative
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                                                                                       /clone_lib="RPC1-11 Human Male BAC"
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/note="assembly_fragment"
12354, 15228
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25808, .28184
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/note-"assembly_fragment"
28285. .31338
/note-"assembly_fragment"
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38419, .42835
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/note-*assembly fragment
52719. .56592
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17361. .26131
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20232, .22587
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56693, .59635
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/note-"assembly_fragment"
4516. .5785
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15329, .17200
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22688. .25707
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    175064
    /organism-"Homo sapiens"
    /db_xref-"Laxon:9606"
    /clone-"RPII-IMI0"

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All repeats were identified using RepeatMasker: html

Http://ftp.genome.washington.edu/RM/RepeatMasker: html

Http://ftp.genome.washington.edu/RM/RepeatMasker: html
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Homo septems clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING.
AC021345
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Mammaiia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90698)
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                                         2872 AACTAGICCCGGCAAAAACCCCGTAATIGCGAGCGAGAGIGAGIGGGGGCCGGGACCCGCA 2931
                                                                                                                                                    24] CCTTCTCCGGAAGGCTTGTCAAGGGTAGGAAAAGAGACAAACACAAACAGAAAA 300
1 AGAGCACAGGCTTTGACCGATAGTAACCTCTGCGCTCGGTGCAGCCGAATCTATAAAAGG
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Homo sapiens, clone RP11-24J9
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/protein_id="AAF69513.1"
/da.xref-"G1:77659513.1"
/translation-"MACWF0!RLJJWKNJTPKRKOTCOLLEVAWPLFIELTJISVRL
SYPPYEQHECHFPNKAMPSAGTLJWVUGJICNANNFCERYFTFGEAPGVVGFFKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens ATP binding cassette transporter : (ARCAL) mkNA, partial cds.
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Francisco, CA 94143-0136, USA
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1 (Lossa: 1 to 647)

Pullinger, C. R., Hakameta, H., Duchateau, P. N., Eng. C., Analysis of haBGO gene 5' end: additional peptide sequence, promoter region, and four polymorphisms

Biochem. Blophys. Res. Commun. 271 (2060) In profess

2 (bases 1 to 697)

Pullinger, C. R., Hakamata, H., Duchateau, P. N., Eng. C., Analysis of habon.
                                                                                                                                                 TACTIGGGCGTTATTGTTTTGTTTCGAGGCCAAGGAGGTTCGGGAAGTGGTGGTTTCG 3195
                                                                   8016 TTTGCTCCTTGTTTTTTCCCCGGGTTCTGTTTTCTCCCCTTCTCCCGGAAGGCTTGTCAAGG 3075
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  12.1 TITGCTCCTTGTITTTTCCCCGGTTCTGTTTCTCCCTTGTCCCGGAASSCTTGTCAAGG
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/note="ABCl"
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3067 TIGICAAGGGGTAGGAGAAAGAGACGCAAACACAAAAGIGGAAAACAG 3114
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                                                                                                                                                  87290
                                                                                                                                                                                                                                                                                                                                                                                  #17289 TIGGGGGTTATTGTTTGTTTGGAGGCCAAGGAGGTTCGGGAAGTGCTTGGGGG 87230
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Pertent: Wo 0170810-A 3 27 SEP-2001;
Hayer Aktiengesellschaft (DE)
                                                                                                                                                                                                                                                              3019 GCTCCTTGTTTTTCCCCGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGT
                                                                                                                                                                                                                                                                            3139 TIGGGCGITATIGITITGITICGAGGCGAAGGAGGCTICGGGAAGTGCTCGGTTTCGAGG
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67055 67947: contig of 893 bp in length 67948 68047: gap of 100 bp 68048 68934: contig of 887 bp in length 68935 69034: gap of 100 bp 69935 69910: contig of 876 bp in length 69911 70010: gap of 100 bp
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100.0%; Pred. No. 9.4e-119;
tive 0; Mismatches 0;
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Pred. No. 1.1e-149;
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                                                                                                                        0; Mismatches
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/db_xref="taxon:9606"
1765 c 1905 q 1756
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AX253452
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99.78;
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Best Local Similarity 100.9
Matches 228: Conservative
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1556 bp mRNA linear PRI 01-AUG-2002 to ATP-BINDING CASSETTE TRANSPORTER 1.
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Aventis Pharma S.A. (FR)
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                                                                                                                                                                                       Homo sapiens
Eukaryoda; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Mominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens placenta cDNA to mRNA, clone_11b:PLACE1
clone:PLACE1002437.
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               linear
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100.0%; Pred. No. 7.1e-115;
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/db_xref+"taxon:9606"
62 c 73 g 43
221 bp
Sequence 4 from Patent WO0183746.
AX351032
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Best Local Similarity
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                                                                                                                                                                                                  Submitted (23-A0G-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mall:genomics*Riri.co.jp, Tei:81-438-52-395, Fax:61-438-22-3966) MEDO human CDNA sequencing project supported by Ministry of International Trade and industry of Japan: coNA hull insert sequencing: Research Association for Biotechnolosy: CNA library construction, 5'- a 3'-end one pass sequencing, and clone selection: Helix Research Institute (Supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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Denefle, P., Rosier-Montus, M.F., Armouid-Requigne, I., Prades, C.,
Naudin, L., Lemoine, C., Duverger, N., Jaye, M., Scarless, G.H.,
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Mammalia: Eutheria; Primates; Catarrhin; Hominidae; Homo.
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Aventls Prantma S.A. (FR)
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Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abol gene and their therapeutic and
diagnostic application
Patent: Wo 0130848-A 70 03-MAY-2001;
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/db_xref="Laxon:9606"
2219 c 2334 g 2635
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/db_xref="taxon:9606"
: 2219 c 2334 g 2635
                                                                                       Aventis Pharma S.A. (FR)
Location/Qualifiers
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[ Chases I to 10442]

Lawn, R.M., Wade, D. and Garvin, M.

Lawn, R.M., Wade, D. binding cassette transporter protein abel Patent: WO 0078972-A I 28-DEC-2000;

CV THERAPEUTICS, INC. (US)
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Eukaryota, Metazoa, Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria; Primates: Catarraini; Hominidae: Homo.
1 (bases 1 to 10442)
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Atp binding cassette transporter protein abc. polypeptides
Patent: WO 0078971-A 128 DEC-2000;
CV THERAPEUTICS, INC. (US)
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/db_xref="taxon:9666"
| 2297 c 2408 q 2835
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/db_xref~"taxon:9606"
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Sequence 1 from Patent WO0078972.
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                                          ACCCAAACACAAAAGTGGAAAACAG 205
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AX060713.1 GI:12406103
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/product="AP-binding cassette transporter 1"
/protein_id="AAF98175.1"
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QQLGCLDHTAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQATRTISRFMECVNLN
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PCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW
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2 (bases 1 to 10442)
Lawn R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Lawn R.M., Wade, D.P., Garvin, M.R., Wang, X., Schwartz, K.,
Dicter, Schools Scholl and Cond. J.J., Vaughan, A.M. and Oram, J.F.

Submitted (16-JUL 2000) Discovery Research, CV Therapeutics Inc.,
3172 Porter Drive, Palo Alto, CA 94304, USA
1. 10442
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10442)
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Pred. No. 6.4e-101;
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/db_xref="taxon:9606"
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291. .7076
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Query Match 6.1%;
Best Local Similarity 100.0%;
Matches 197; Conservative 0
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PEKEVGEVGETALSTVAKGENSVVLTSTSHSHEEFEALTTHMATNYNGREKCIJGSVQHLK
NRFGGGYTIVYRLAGSNPLIKPVJEFFGLAFFGSVLSERFRANTGYGLSSSISSLAKE
FSILSGSKKRLHIEDYSVSQTTLDAVPVNFAKOJSGDGHLKG,SLHKNGTVVJVAVLT PAT 22-JAN-2001 SRANLAAACGGI IYFTLYLPYVI.CVAWQDYVGFT.KIFAS.LLSPVAFGFĞCEYFALFE EQGIGVQWDNLFRSPVEE.XGFNLTTSISMMLFDTFLYGVMTWYLEAVFPGQYGIPRPW RILDGGGQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKM ċ Eukaryota, Metazoa, Chordata, Graniata, Verrebiata, Eule.costumi: Mammalia, Eutheria, Primates, Catarrhini, Huminidue: Homo. 1 (bases 1 to 10474) 30.57 ETHER THE FITTER FOR A STATE OF THE STATE OF O: Caps 297# GGANTICOGGGGACCACAAGAGGGGTTCTCAGGCTACTTTGCTCTTTGCCAG Lawn, R.M., Wade, D. and Garvin, M. Requiation with binding cassette transporter protein abol Patent: WO 0078972-A 7 28 DEC 2000; CV THERAPEUTICS, INC. (US) undels Tear: Ouery Match 6.1%; Score 197; DB 9; te Best Local Similarity 100.0%; Fred. No. 6.4e 101; Matches 197; Conservative 0; Mismatches 0; UNA 2408 g 2835 t /organism "Homo saptens" /db\_xref="taxon:9605" a 2305 c 2416 q 2844 AX060719 10474 hp. Sequence 7 from Patent WC0078972. AX060719 Location/Qualitiers SFLQDEKVKESYV" AX060719.1 GI:12406108 3098 ACAAAAGTGGAAAACAG 3114 ACAAAAGIGGAAAACAG 197 10474 2297 C Homo sapiens human. DEFINITION ORGANISM BASE COUNT 181 RESULT Z5 AXU60719 ACCESSION REFERENCE AUTHORS JOURNAL. KEYWORDS VERSION ORIGIN SOURCE 3 ŝ ŝ ò 3 3 3

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 10474)
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1 Regulation with binding cassette transporter protein abc)
Putent; WO 0078972-A 9 28-DEC-2000;
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Best Local Similarity 100.0%; Pred. No. 9.6e-96;
Matches 188; Conservative 0; Mismatches 0;
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/db_xret-"taxon:9606"
a 2304 c 2415 q 2844
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AX560899 1 strillatur.23s
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Location/Qualifiers
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222 GAAAACAG 229
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                                        Eukaryota, Metazoa, Chordata, Graniata, Vertekralu, Euteleostomi, Mammalia, Eutherla, Primates, Catarinini, Hosniddo, Homo.

[Chases I to 10474]

Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.

Lawn, R.M., Wade, D., Oram, J.F. and Garvin, M.

Patenti, W. 0078971-A 28 ibEC-2008;

CV THERAPEUTICS, INC. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Enkaryota, Metazoa: Chordata, Prantata, Verebrake: Borehesskumin
Mammalia, Eutheria, Primates; Calatthin, Raminidae; Bome.
1. (bases 1 to 10474)
                                                                                                                                                                                                                                                                                                                                                                           3047 TCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGAGAAAAGAGAGGAAACGCAAAAAGTG 31.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2927 CCGCAGAGCCGAGCCGACCCTTCTCTCCCGGGCTGCGGAGGGCAGGGCCGGGAGGCTCCG 2986
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CV THERABUTICS, INC. (US)
Location/Qualitiers
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9.6e-96;
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/db_xref="taxon:9606"
2305 c 2416 g 2843
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/db_xref="taxon:9606"
2304 c 2415 g 2644
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AX060900
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100.0%; Pred. No.
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Matches 188; Conservative
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Discer 1 to 90698)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barran, N., Beckerly, R., Beda, E., Brown, A., Burkett, G., Castle, A. Bardah, L., Barnan, N., Beckerly, R., Beda, F., Googel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Domino, M., Doyle, M., Fenetror, J., Ferreira, P., Fitzhugh, M., Forrest, C., Gage, D., Galagan, J., Ferreira, P., Fitzhugh, M., Forrest, C., Gage, D., Galagan, J., Radiada, A., Mchand, J.C., Johnson, R., Jones, C., Landers, T., Leborckky, J., Lewine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McGonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, C., Liu, G., Locke, K., McGonald, P., Marquis, J., Marens, L., Morrow, J., Naylor, J., Norman, C., Liu, G., Locke, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Elley, R., Fothman, D., Roy, A., Sanios, R., Senios, Severy, P., Spencer, B., Stange-Thoman, D., Ye, W. J., Stoje-Inovic, N., Stange-Thoman, D., Ye, W. J., Stoje-Thoman, D., Ye, W. J., Myman, D., Ye, W. J., Limer, A., Wassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Limer, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Limer, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., M. J. 200 this sequence version replaced gi:6705761.

All repeats were identified using RepeatMasker. html

Christ, Code, Willed Code, Willer, MIT Center for Genome Code, Willer, Code, Willer, Code, Willer, Will R., Conter, Willer, Willer, Willer, Code, Conter, Willer, Willer, MIT Center for Genome Code, Willer, Code, Willer, Code, Willer, Willer, Code, Willer, Code, Willer, Willer, Willer, Code, Willer, Willer, Code, Willer, Colling, Colling, Code, Code, Willer, Code, Willer, Code, W
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases i to 90698)
ACU21345 90698 bp DNA linear HTG 1
Homo sapiens clone RP11-24J9, LOW-PASS SEQUENCE SAMPLING:
AC021345
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* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
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1011 1873: contig of 863 bp in length
1874 1973: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-24J9
Unpublished
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Web site: http://www-seg.wi.mit.edu
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of 851 bp	878		160 bp of 843 bp	90	100 bp	100 pb	of 90d tp 100 bp	80.00	100 pp of 904 bp	100 bp	100 b	<u> </u>	_	7.	100 Up of 878 pp		- a - b	0.0	of 901 bg 100 bp	~r. <sup>4</sup>	0.5	100 bp of 886 bp	1001	~	of 889 bp	, c	da Zuk to	100 pb 01 866 bp	100 pp.	a.	150	100 E	of 883 bp 100 bp	906	146 pp of 899 bp	100 bp	ر 0	of 888 hp	of 898 bp	100 bp	1001	ot 882 bp	्र ४३८ bp
2824: contig	3802: 0	4816: 0	<b>-</b> -	59: gap o 6764: c	64: yap o	47: gap of	8755 55: qa	9753:	53: gap o 10757: c	857: g	832: gap of	12739 839: q	13710: C	14684: CO	784	762: gap o 16677: co	777: gap of	1/6/8: Cont 778: gap of	18679: cont. 779: gap of	19632: c	20634: co	734	720: qap ot	679: gap of	23568: 668: 44	24554: co	25521: co	621: 2648	587	564: gap of	566: gap of	29464: contra 564: gap of	3044 547:	31453: co	ი ო ი	55	7: gap of	00 (	35433	3: 98	gap of	3742 522:	38402: CO
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	Gaps
length	Length 90698; ; Indels 0,
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38502; gap of 100 bp 39880; contig of 878 bp 39880; contig of 878 bp 40407; contig of 927 bp 40407; contig of 927 bp 42495; gap of 100 bp 42499; contig of 889 bp 44356; contig of 889 bp 44356; contig of 889 bp 44356; gap of 100 bp 4323; contig of 889 bp 4323; contig of 889 bp 5325; contig of 889 bp 6325; contig of 881 bp 6325; contig of 8825 bp 6325; cont	4.7%; Score 152; DB 99.2%; Pred. No. 5.8e-vative 0; Mismatches
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Location/Qualifiers

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Eukaryota, Metazoa, Chordata: Craniata, Vertebrata, Euteleostomi;
Mammalla: Eutheria; Primates, Catarrhini, Hominidae: Homo.
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         synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 446)
Denefle.P., Rosier-Montus.M.F., Arnould-Requique.I., Prades.C.,
Maudin.L., Lemoine.C., Duverger,N., Jaye.M., Searfoss.G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abol gene and their therapeutic and
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100.0%; Pred. No. 4.1e<sup>-55</sup>;
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Patent: WO 0130848-A 3 03-MAY-2001;
Aventis Pharma S.A. (FR)
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Aventis Pharma S.A. (FR)
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/db_xref-"taxon:9506"
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AX351034
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AX127764
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Best Local Similarity 100.00
Matches 117; Conservative
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AX127764
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 9741)
Denefle,P., Rosier-Montus,M.F., Arnould-Regulgne,I., Prades,C.,
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Nucleics acids of the human abcl gene and their therapeutic and diagnostic application
Patent: EP 1096012-A 3 02-MAY-2001;
Aventis Planma S.A. (FR)
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                                                                                                                   Score 92; DB 6; L4 Pred. No. 1.1e-40;
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/db_xmef 'daxon:32630'
/note-"Oligonuclectide Primer'
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonuclectide Primer"
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100.0%; Pred. No. 1...
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Sequence 69 from Patent WO0130848.
AX127830
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Sequence 3 from Patent EP1096012.
AXI39751
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1 (bases 1 to 446)
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Eukaryota, Metazoa, Chordata, Craniata: Vertebrais: Euteleostomis
Mammalia: Eutheria: Primates, Caturrhini; Hominidae: Bomo.
1 (bases I to 9741)
Denotle.P., Rosier-Montus.M.F., Atmoslaf-Reavigno.I., Prades.C.,
Naudin.L., Lemoline.C., Duverger,N., Jaye.M., Sentfoss III, 64. N.,
Nemaley.A., Brower, H.B., and Denot.M.,
Nucleics acids of the human abcl gene and their therapertic and
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Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Searfoss,G.H.,
Remaley,A., Brewer,H.B. and Dean,M.
Nucleic acids of the human abol gene and their therapeutic and
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100.0%; Pred. No. 1.5e-40;
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Patent: EP 1096012-A 69 02-MAY-2001;
Aventis Pharma S.A. (FR)
                                                                                diagnostic application
Patent: WO 0130848-A 69 03-MAY-2001;
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AX139817
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/db_xref="taxon:9606"
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Direct. B. Fasman, K., Mckernan, K., Nusbaum, C., Richardson, P., Butrer, B., Fasman, K., Mckernan, K., Nusbaum, C., Richardson, P., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Boutweli, C., Lyrne, S., Cantu, C., Castle, A., Cerny, J., Cooke, P., Daly, M. J., Depayre, E., Lewon, K., Dewar, K., Donelan, L., Dukette, B., Etemadi, S., Ferreira, P., Forrest, C., Punke, R., Gage, D., Gardyna, S., Gensheimer, S., Gerajgery, K., Glimartin, T., Gray, D., Hagos, B., Hartis, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Linton, L., MacKenzie, J., Marquis, N., McEman, P., McGurk, A., Meidrim, J., Molla, M., Morris, W., Morman, R., Raley, K., Roberts, D., Ralin, B., Peterson, K., Ranganath, S., Riley, R., Roberts, D., Stange-Thomann, N., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Ye, W. J., Zentseva, I., Zhao, J. and Zody, M., Wiveler, J., Wu, Y., Ye, W. J., Zentseva, I., Zhao, J., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126295 bp DNA linear PRI 02-SEP-1998 Homo sapiens chromosome 17, clone HRPC843B9, complete sequence. AC004139
AC04139 HTG.
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Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J.,
Boutwell, C., Brown, A., Castle, A., Cerry, J., Colangelo, M.,
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Devon, K., Dewal, K., Donelan, L., Ferreira, P., Fitzlery, W.,
Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, M.,
Jacotori, L., Jones, C., Rann, L., Karatas, A., Lehoczky, J.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
Meldrim, J., Molia, M., Morris, W., Morrow, J., Mychaleckyj, J.,
                                                                                                Rosier Montus, M.F., Prades, C., Lemoine, C., Naudin, L., Denefle, P., Brewer, B., Duverger, N., Remaley, A. and Santamarina Fojo, S. Regulatory nucleic acid sequences of the abol gene Patent: WO 0183746. Al 0 08-NOV-2001; Aventis Pharma S.A. (FR)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryoja, Metazoa: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3023 CTIGITITI PCCCCGGTTCTGTTITCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 3082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTTGTTTTTTCCCGGGTTCTGTTTTCTCCCCTTCTCCGGAAGGCTTGTCAAGGGGTAGGA 60
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1 (bases 1 to 126295)
Birren. R., Linton.L., Nusbaum,C. and Lander,E.
Unpublished
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7, 1.5e-40;
0;
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illarity 100.0%; Pred. No. 1.5
Conservative 0; Mismatches
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Best Local Similarity
Matches 92; Conserv
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Nahí,R., Naylor,J., Niloff,M., O'Connor,T., G'Donnell,P., Pavlin,B., Peterson,K., Riley,R., Roberts,D., Roy,A., Severy,P., Stange-Thomann,N., Stilwell,J., Stojanovic,N., Store,C., Subrananian,A., Testaye,S., Tichovolsky,M., Torruella-Miller,I., Vaskillav,H., Vo.A., Wagner,A., Wheeler,J., Wu,Y., Wyran,D., Ye,W.J., Zhao,J. and Zody,M.  TITLE Direct Submission JOURNAL Submitted (02-SEP-1998) Whitehead Institute/M.T Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 2, 1998 this sequence version replaced gi:1451870, All repeats were identified using RepeatMasker: Smit, A.F.A. 6 Green, P. (1996-1997)	http://ftp.genome.washington.edu/HM/RepeatMasker.html. Location/Qualifiers 1. 126295 /organism="Homo sapiens" /organism="Homo sapiens" /chromosome="17" /map="17" /clone="HRPC843B9" /clone="HRPC843B9" /clone="HRPC843B9"	repeat_region complement(235, .410) /rpt_family="MERSA" /rpt_family="MERSA" /rpt_family="MERSA" /rpt_family="MIR" /rpt_f	repeat_region 7784544  topeat_region /rpt_family="L2"  topeat_region complement(5068. 5364)  repeat_region complement(64036675)  repeat_region /rpt_family="MIR"  repeat_region /rpt_family="MIR"  repeat_region /rpt_family="MIR"  repeat_region complement(7735734)  repeat_region complement(77357340)  repeat_region complement(77357340)  repeat_region complement(77357340)  repeat_region complement(77357340)  repeat_region complement(77357340)	repeat_region complement(78837988)  repeat_region / rept_family="Tigger1"  complement(78998597)  repeat_region / rept_family="FLAM_C"  repeat_region / rept_family="FLAM_C"  repeat_region / rept_family="Alusx"  repeat_region / rept_family="Alusx"  repeat_region / rept_family="Alusx"  repeat_region / rept_family="Aluger1"  repeat_region / rept_family="Tigger1"  repeat_region / rept_family="Tigger1"  repeat_region / rept_family="Limc2"  repeat_region / rept_family="Limc2"  repeat_region / rept_family="Limc2"  / rept_family="Limc2"

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ap of 100 bp contig of 10024 bp in length
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$ $8184: contig of 2177 bp in length
$ 50786: contig of 2402 bp in length
$ 60886: gap of 2402 bp in length
$ 60807: contin **
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156318 156417: qap of 100 bp
156418 186889: contig of 30472 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         66708 66807; gap of 100 bp 66808 92202; contig of 25295 bp in length 92103 92903; contig of 7707 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ap of 100 bp contig of 11174 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132374 132473; qap of 100 bp

134474 134930; contig of 2457 bp in length

134931 135030; gap of 100 bp

135031 139301; contig of 4271 bp in length

135031 139301; contig of 4271 bp in length

135302 139401; gap of 100 bp
              22720; gap of 100 bp 2993; contig of 7243 bp in length 30063; gap of 100 bp in length 40687; contig of 10024 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125960 126059; g4p of 100 bp 126060 128749; contig of 2690 bp in length 128750 128849; g4p of 100 bp 128850 132373; contig of 3524 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144449 144548: qap of 100 bp
144549 147074: contiq of 2526 bp in length
147075 147174: qap of 100 bp
147175 156317: contiq of 9143 bp in length
                                                                                                p of 100 bp contig of 4251 bp in length
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22721. .2963

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30064. .40087

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40188 .44438
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1. 4849
/note="assembly_tragment:01920
fragment_chain:1"
4950. .22620
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49061. .56007
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                                                                                                40187: gap of
44438: con
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Mammalia; Eutheria: Rodentia; Sciurodnathi; Miridac; Murinde; Mus.
1. (bases 1 to 186889)
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Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Binxton,
Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Binxton,
Cambridgeshire, CBIO 15A, UK. E-mail enquirities:
Rumquery@sanger.ac.uk Clone requests: clonercquest-sanger.ac.uk
On Jul 2, 2002 this sequence version replaced qt.2(*58136.
                                                                                                                                                                                                                                                                                                                                                                1017 GATCTCGACTCACTGTAACCTCTCCCGGGGTTCAAGCGATTCTCCTGACTAGACTCT 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: XGAP4: version 4.5
Assembly program: XGAP4: version 4.5
Consensus quality: 17959 bases at least 04:
Consensus quality: 179463 bases at least 07:
Consensus quality: 182069 bases at least 07:
Insert size: 184589; sum-of-contiqs
Insert size: 184589; sum-of-contiqs
Ouality coverage: 4.72x in 020 bases; sum-of-contiqs quality
coverage: 4.82x in 020 bases; sum-of-contiqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as It is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                Length 125295;
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                                                                                                                                                                                                                                                            2.0%; Score 65; DB 9; LA
100.0%; Pred. No. 6.1e-25;
Live 0; Mismatches 0;
        /rpt_family="LIME3A" 35874) 35830, 35906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                       .376293
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/rpt_family-"Aluxb8"
complement(35504. .39
                                                                                                                                                       /rpt_family="Alusg" 36517, 36682 /rpt_family="AluJo" complement(36689, 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL807243,5 G1:21668234
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                          /rpt_family-"AluJo"
35907. .36194
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                                                                                                                 /rpt_family~"Aluy"
36204. .36516
                                                                                                                                                                                                                                                                                                  65; Conservative
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                                                                                                                                                                                                                                                                                 Best Local Similarity
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Db 31175 CTGAG 31179
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                   copeat_region
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ALBO7243/r
LOCUS
                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
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KEYWORDS
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Direct Submission
Submitted (20-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
HO 63108, USA
Waterston R. H.
Direct Submission
Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
on Feb 16, 2001 this sequence version replaced 91:11761497.
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MC. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The RCI of Induces HAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenc, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is RPI1-62B4. Actual start of this clone is at base position 1 of RPI1-389E17; actual end is at base position 206966 of RPI1-389E17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this conne. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all requons were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by sequence from more time none subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: Sapiens@Watson.wustl.edu
Centert: Surmary Statistics
Center project name: H_NH0389E17
                                                                                                                                         2 (bases 1 to 206966)
Ang, K., Maupin, R. and Ureta, M.
The sequence of Homo sapiens BAC clone RP11-389E17
Unpublished
                                               Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://bacpac.med.buffalo.edu)
1 (bases 1 to 206966)
Sulston, J.E. and Waterston, R.
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                                                                                                                                                                                                                                        3 (bases 1 to 206966)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 (bases 1 to 206966)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 206966
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                    AUTHORS
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MEDLINE
     KEFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae, Bomo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Homo sapiens BAC clone RPIL 389E17 from 4, rompletor sequence.
ACO21850
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156418. 186889
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/note="assembly_tragment:00358
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7000e="assembly_fragment.00557"

144549, 147074
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                    /note="assembly_tragment:00965
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58385. .60786
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/note-assembly_fraqment:01792
fragment_chain:2*
92203. .99909
                                                                                                                                                           //note="assembly_fragment:00374
fragment_chain:2"
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Best Local Similarity 100.0
Matches 61: Conservative
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  misc_feature
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ORGANISM
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AC021850/c
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repeat\_region

Massucerius ATP-binding cassette 1, sub-family A, member 1 (Abcal) AF267263 ö Mus musculus.
Mus musculus
Bukaryotaya Metazoa, Chordata, Craniata, Vertebrata: Euteleostomi;
Bukaryotaya Metazoa, Chordata, Sciurognathi; Muridae, Murinae, Mus.
1 (Lases 1 to 22852)
Vittie, Taveffer,L., Chia,S., Yang,X., Rubin,E. and Chena,J.E. Length 206965; 0; Indels Query Match 1.9%; Score 61; DB 9; Le Best Local Surjacity 100.0%; Pred. No. 1.3e-22; Matches 61; Conservative 0; Mismatches 0; /rpt\_family="tRNA-Cys-TGC" 29979, .30116 /rpt\_tamily-"MER1\_type" 27597. .27619 /rpt\_tamily="AT\_rich" 29420. .29635 /rpt\_tamily="AT\_rich" 40735. .40755 /ipt\_family="AT\_rich"
28709. .28781 /rpt\_family-"At\_rich" 14635. .34825 /rpt\_family="AT\_rich" 35645, .35691 /rpt\_family="AT\_rich" 40826. .41030 /rpt\_family="(cA)n" 46784, .37028 /rpt\_ramily="Ll" 37106, .37171 /rpt\_tamily="AT\_rich" 37582. 38445 /rpt.ramily-"ERVL" 39128. .39148 /rpt\_family="MIR" 24706, .24903 /rpt\_family="MIR" 26677, .27207 7/100, 37/71 //pt\_family-"L1 17/81, 37/2 /rpt\_tamily="Alu" 29865. .29898 /rpt\_family~"CR1" 33594. .34090 /rpt\_family="MIR" 30773, .31036 /rpt\_family="Ll" 34248, .34248. /rpt\_family="f.1" 35013. .35078 /rpt\_family="L2" 31039, 31722 /rpt\_family="1.2" 32160. .32333 AF287265.1 GI:11611824 repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat tegion repeat\_region 45669 C 45669 Qy 1077 C 1077 DEFINITION OPGANISM RESULT 59 AF287263 ACCESSION REFERENCE VERSION KEYWORDS SOURCE 1.0000 2

AUTHORS

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/rpt\_family "L1"
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23028, 23085

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/rpt\_family="AcHobo" 23878, 23976

repeat\_region

repeat\_region

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NNTEEDVOTFYDNSTTPYCNOGMKNIESSPISKIIWALKPLINGKILYTPUTPATRO
VMAEVMYTPOELAVFHDIEGMWEELSPOIMFPMENSJEMDIVYTILDSKGNDOFWEOK
LDGLDMTAQDIMAFLAKNPEUVQSFNGSVYTWERAFNGATAGTISKFMECVNINKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IKDGYMDPGPRADPPEDMRYVW3GFAY1,0,0VVEQA11RVC,FGSEKKTGVYVQGMPYPG
YVDDIFLRVMSKSMPLPMTIAMFYSVAV11KSTVYFKBARI,KETMKIMGLDNGTIMES
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SLPRSTVDSLLQANVGLQKVFTQGYYQTHTASLGNGSKLEBTTQLGDABVSALGGLPRK
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ANLAAACGGIIYFTLYLPYVL-VAWQDYVEFSIKIFASILLSEVAFGESTFFFALEEG
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                                                                                                                                                                                                                                                                                   2 (bases 1 to 278572)
Gluty., Caveller., Chit.S., Rubin.E. and Cheud.J.-F.
Direct Submission
Submitted (14-JUL-2000) Genome Science Department, Lawrence
Externey National Laboratory, 1 Cyclotron Ed. MS 84-171, Berkviey,
CA 94720, USA
Human and mouse ABCAl comparative sequencing and transgenesis studies revealing novel regulatory sequences 73 (1), 66-76 (2001) 21251004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | John (1978) | John (1978) | John (1974) | 
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2.5096.
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.202996, 254355,
.206842, 257561,
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157459. 157664.158200. 156475.158421
160617. 160838.161750. 161994.156075.
164646. 164817,165738. 165869.15771.
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87184; .210783
/gene="Abcal"
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135582, 135758,147083,
152367, 152506,152845,
157459, 157664,158200,
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202114. . 202176, 202890.
205427. . 205558, 206749.
208135. . 208378, 209638.
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1. .278572
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/codon_start-1
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                                                                                                                     JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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Dupublished

Updates 1 to 44897)

Shiren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Bukkgaiter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,

Ferreira, P., Fitzhugh, W., Gag, D., Galagan, J., Gardyna, S.,

Gonde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,

Hagos, B., Heaford, A., Hotton, L., Hulme, W., Illev, I., Johnson, R.,

Jones, C., Mandton, K., Karatas, A., Kells, C., Larkoque, K.,

Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lu, G.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

MacLean, C., Mihova, I., Mikoya, I., Maylor, J., Naylor, J., Naylor, J.,

Norbu, C., Nermar, C.H., Connor, T., O'Donnell, P., O'Neil, D.,

Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
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VSCLKKEDSVSQSSSDAGLGSDHESDTLTIDVSAISNLIRKHVSEARLVEDIGHELTY
VLYYEAAKEGAFVELFHEIDDRLSDLGISSYGISETTLEEIFIKVAEESGVDAETSDG
DGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSSIRQN
LGVCPQHNVLFDMLTVEEHIWFYARLKGLSEKHVKAEMEQMALDVGLPPSKLKSKTSQ
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Mammaila: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Nusbaum, C. and Lander, E.
Homo sapicus chromosome 8, clone CTD-2319014
Unpublished
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100.0%; Pred. No. 1.3e-22;
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Matches 61; Conservative
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TITLE
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if 704 bp in length
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32: contig of 718 bp in length
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3 31591; contig of 759 bp in
2 31691; gap of 100 bp
9 32398; contig of 607 bp in
9 33145; contig of 747 bp in
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134825: contig of 747 bp in

6 34925: gap of 100 bp

13564: contig of 739 bp in

5 35764: gap of 100 bp

5 36499: contig of 735 bp in

0 36599: gap of 100 bp

17448: contig of 749 bp in

9 47448: contig of 249 bp in
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10811; con
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16563: con
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11635: con
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13349: con
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Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Koman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Scaman, S., Severy, P., Sponcer, B., Stange, Ticmann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triqilio, J., Vassiliev, R., Zalnoun, J., Zalnoun, J., Zalnoun, J., Zalnoun, S., Zalnoun, J., Zalnoun, S., Zaln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (30-JUL-2002) Whitehead institute/Mil Conter for Genome Research, 320 Charles Street, Cambridge, MA 02141, 18A on Jul 30, 2002 this sequence version replaced quit7149709.

All repeats were identified using RepeatMasker:
Smit, A.E.A. & Green, P. (1996-1994)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                  Submitted (29.NOV-2001) Whitehead fistitute/M.T Center for Gasome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 44897)
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5753: contig of 723 bp in length
3: gap of 100 bp
6627: cow*in
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contig of 755 bp in
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Center clone name: 2319_0_14
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$930: gap of 100
$753: contist
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7449: cor
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Homo sapiens chromosome li cione CED-2028GES map 11. LOW-PASS
ACCHENCE SAMPLING.
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                                                    length
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        38207 38306; gap of 100 bp 38307 39039; cont.g of 732 bp in. len 39039 39138; cap. of 100 bp 39139 39800; gap of 100 bp 3981 39980; gap of 100 bp 40732; cont.g of 752 bp in. len 40733 40832; cont.g of 752 bp in. len 40733 40832; cont.g of 756 bp in. len 41539 41639; cont.g of 706 bp in. len 41539 41639; cont.g of 758 bp in. len 41539 41639; cont.g of 758 bp in. len 41539 41639; cont.g of 758 bp in. len
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism."Homo sapiens"
/db_xref*"taxon:9606"
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contig of
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HTG: HTGS_PHASEO.
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Direct Submission
Submitted (24-3M1-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fip.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                configs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing reads that have not been assembled into
                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 442: 9ap of 100 bp 1
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13187: contig of 701 bp in length
13287: gap of 100 bp
13988: contig of 701 bp in length
14088: gap of 100 bp
14795: contig of 707 bp in length
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f 689 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 717: contig of 717 bp in length
718 817: gasp of 100 bp
818 1525: contig of 708 bp in length
1526 1625: gasp of 100 bp
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contig of 640 bp in length
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3845: contig of 695 bp in length
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f 692 bp in length
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682 bp in length
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if 704 bp in length
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Web site: http://www-seq.wi.mit.edu
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of 632 bp i
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17961: contig of 706 bp
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5369: contig of
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4577: con
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6151: con
6251: qap of
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17155: con
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5 2365: GPT
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19477 19576: gap of 100 bp in length 19577 20274: contig of 698 bp in length
                                                                                                                                                                                                                                                                                  31: gap of 100 bp
28232: contig of 761 bp in lenath
32: gap of 160 bp
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100 bp
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706 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33927; gap of 100 bp
34646; contig of 719 bp in length
34746; gap of 100 bp in length
35451; contig of 705 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37877; qap of 100 bf
38587; contig of 716 kp in length
18687; gap of 100 bp
39375; contig of 668 bp 16 length
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701 bp in length
                                               20275 20374: gap of 100 bp
20375 21074: contig of 700 bp in length
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contig of 693 bp in length
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22680: contig of 713 bp in length
                                                                                                                                                                             27: gap of 100 bp
25032: contig of 705 bp in length
                                                                                                                                                                                                                               38: qap of 100 bp
26651: contig of 713 bp in length
                                                                                                                                                                                                                                                                                                           32: gap of 100 bp
29032: contig of 700 bp in length
                                                                                                                                                                                                                                                                                                                                  29132: gap of 103 bp
29818: contig of 706 bp in length
29938: gap of 100 bp
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36993: contig of 649 bp in length
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contig of 706 bp in length
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27431: contig of 680 bp in length
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contig of 704 bp in
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41749: contig of 663 bp in
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42551: contig of 702 bp in
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contig of 673 bp in
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31567 32272; contig of
32273 32372; gap of 1
gap of 1.6: contig of
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46513: con
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Loughitted (14.5EP-1998) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 18, 1998 this sequence version replaced gi:3550203.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS931E15 81874 bp DNA linear PRI 23-NOV-1999 Human DNA sequence from clone 931E15 on chromosome X425. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HOP/ChrX
931E15 is from the library RPC15 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2
IMPORIANT: This sequence is not the entire insert of clone 931E15.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neighbouring submissions.

The true left end of 424312 (282207) is at 36643 in this sequence. The true right end of 506G2 (282213) is at 37431.

Location/Qualifiers

1.81874
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 81874)
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Score 58; DB 2; Lengt.,

And No. 6e-21;

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Direct Submission
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Source

FEATURES

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	/organism-"Homo sapiens" /db_xref-"taxon:9606"	repeat_region
	/chromosomex-/map=#q25	misc_feature
	/clone_11b-"RP3-91E15" /clone_11b-"RPC1-5"	repeat_region
repeat_region		repeat_region
repeat_region	Complement(228531) Ablosx repeat: matches 292; of consensus" con	repeat_region
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repeat, region	702. 1802 Anote-Alusp repeat: matches 1 .4.2 of consensus" 1808. 1728	repeat_region
refred_requon	/note-"FRAM repeat: matches 5166 of consensus"	repeat_region
misc_reature	Complement(135), 1554) /note-"match: STS G05254"	repeat_region
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repeat_region	<pre>//octe-/aludb repeat: matches i302 3: consensus"</pre>	repeat_region
	complement(4220, .4037) /note-"Aludo repeat: matches 300, .1 of consensus"	misc_feature
	47015004 /note="Aludo repeat: matches 2, .302 of consensus"	misc_feature
	5170. 5497 //octe="11 repeat: matches 3627. 3996 of consensus"	repeat_region
	54965043 /note="AluSq repeat: matches 1146 of consensus" //www.matches 1146 of consensus	repeat_region
	Joseph 1994   John Parkers   John Pa	repeat_region
	7930ott. /note="AluSg repeat: matches 133200 of consensis"	misc_feature
	01500393 /oote="Li repeat: matches 3985, .4249 of consensus" /oote	misc_teature
	00290979 /note="L1 repeat: matches 4377473; or consensus"	repeat_region
	6978. 7073 /note="MER2 repeat: matches 195 of consensas"	repeat_region
	Complement(7078, 77334) /note="MRR2" repeat: matches 345, 284 or consensus"	repeat_region
repeat region	7238. 7875 7700te**Ll repeat: matches 47285161 or consensus** 7730	repeat_region
repeat_region	/o/6. //yoy /note="Alux repeat: matches 1293 of consensus"	repeat_region
repeat_region	79708091 /note="L1 repeal: matches 51506270 o: consensus"	repeat_region
repear_region	00440350 /note="AluY repeat: matches ]3Un of corsensus" of the core	repeat_region
repear region	04000013 /Aote-*LLMB3 repeat: matches 47276 of consensus*	repeat_region
repeat_region	00100733 /note="AluJo repeat: matches 212! of consensus" 0012 0016	repeat_region
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ropost teodor	/note="Allo repeat: matches 2300 of consensus"	repeat_region
notes - anoder	Jose "Alujo repeat: matches 87299 of consensus"	repeat_region
notest_region	5505. 3500. 5506 - Angor repeat: matches 1302 of consensus" 5606 - Angor	repeat_region
repeat_region	/note="Likaly repeat, matches 297, .919 of consensus"	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
	Comprehence (1007). The comprehence of consense.	ופואפר די בא זפון
repear Teaton	70710. 11004 //oce="Albust repeat: matches 7301 of consensus"	repeat_region
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On Sep 27, 2000 this sequence version replaced at 6006528.

On sequence assembly date is compared troin overlapping clone differences are found these are annotated as variations together with a note of the overlapping clone, as we sutchin substitution annotation may not be found in the sequence substitution only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases.

Em: EMBL: Sw.: SWISSPRYP: Fr.: TREMBL: WP. WEMMER: information on the WORMPRP database can be found at the WEMPER: information on the WORMPRP database can be found well-4702 it may be sequence is not the entire insert of clone RPI-4402 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The frue left end of clone RPI-24702 is at 1 in this sequence. The true right end of clone RPI-8918 is at 98261 is this sequence. This regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30): an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were aborded by at least, one plasmid subscione or more than one MBS autoclose; and the assembly was confirmed by regions were propered to be found the assembly was confirmed by regions were propered to be found the assembly was confirmed by regions were propered to be found the assembly was confirmed by regions were propered to be found the assembly was confirmed by regions were propered to be found the assembly was confirmed by regions were propered to be found to be assembly was confirmed by the found to be an one plasmid subscioned to the plasmid subscioned to the plant of the plant of the plant of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSDJ247C2 98360 bp DNA linear PRI 03-AUG-2001 Human DNA sequence from clone RP1-247C2 on chromesome 11pl3 Contains STSs and GSSs, complete sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertefrata, Euroleostomi,
Mammalia, Futheria, Primates, Catarriini, Hominidae, Homo.
1 (bases 1 to 98360)
Wallis, U. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-AUG-2001) Sanger Centre, Hinxton, Campildoeshire,
CB10 15A, UK. E-mail enquiries: humquerydsapycr.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 39890 CTGCCCACCTTGGCCTCCCAAATGCTGGATTACAGGCATGAGGCACTGAGGCCAGG 39833
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1187 CIGCCCACCTIGGCCTCCCAAAGIGCTGGGAITACAGGGATGAGGGAGGAGIAGIGGGGGC 1244
32041. 32319

/note-"Alusz repeat: matches 1. .287 of consensus"
complement(32381. .33599)
/note-"MLT2_internal repeat: matches 4572. .3316 of
                                                                                                                                                                             /note="AluJo repeat: matches 1, .372 of consensus"
34020, 34321
                                                                                                                                                                                                                                       /note="AluJb repeat: matches 1, .301 of consensus"
complement(34388, .34933)
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                                                                                                                                                                                                                                                                                                                                 Length 81874;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                    Score 58; DB 9; L
Pred. No. 6.2e-21;
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VECTUR: pCYPAC2.
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/db_xref*"taxon:9606"
/chromosome*"11"
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AL049713.20 GI:10334639
HTG.
                                                                                                                                                      33806
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                                                                                                                      33603. .33
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                                                                                                                                                                                                                                                                                                                                                                    Similarity 100.
58; Conservative
      repeat_region
                                                                                                                                                   repeat_region
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                                                                                                                                                                                                                                                                                                                                                                    Local
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HSDJ247C2/c
LOCUS
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TITLE
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42053. .42372
/Hote="Charliela repeat: matches 778. .1137 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Charliela repeat: matches 277. .769 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"31 copies 2 mer gt 91% conserved"
38956. 39215
/note-"Charliela repeat: matches 28. 281 of consensus"
40351. 40840
                                                                                                                         .2215 of consensus"
                                                                                                                                                                                                 .6162 of consensus"
                                                                                         .2191 of consensus"
                                                                                                                                          4265. .5286

/note="LiPA11 repeat: matches 2215. .3216 of consensus'

/note="LiPA11 repeat: matches 3216. .6162 of consensus'

10697. .10906

/note="LiMEC repeat: matches 2142. .1979 of consensus'

1202. .11493
                                                                                                                                                                                                                                                                    .2279 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note*"MLT1A2 repeat: matches 92. .374 of consensus" complement(17710. .18372)
                                                                                                                                                                                                                                                                                                                                                                                                                                              15930. 15955
/notc-"13 copies 2 mer tg 92% conserved"
15984. 1707
/note-#MIT1Az repeat: matches 1. .92 of consensus"
17380. .17654
                                                                                                                                                                                                                                                                                                                                /note="13 copies 2 mer gt 100% conserved"
                                                                                                                                                                                                                                                                                            //oct- 32 copies 2 mer cc 68% conserved 14618. 15078
                                                                      3773. .3810
/note-"iJPAll repeat: matches 2154.
                                                                                                            4956. .3992
/note="LiPAll repeat: matches 2180.
                                                                                                                                                                                                                                                                /note="LIMEc repeat: matches 1978.
13794. .13857
complement(627, .983)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"match: GSS: Em:AQ485260"
1844. .18750
/note-"match: GSS: Em:AQ545989"
complement(20477. .21170)
/note-"match: GSS: Em:AQ488664"
complement(20761. .21177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AQ669825"
complement(25626. 26158)
/note="match: GSS: Em:AQ505438"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"match: STS: Em:AU046429"
complement(38660. .38777)
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/note-"match: STS: Em:AU048503"
38620. 38772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match: GSS: Em:AZ398168"
38685. .38746
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   complement (627
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ACCESSION
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Human DNA sequence from clone RPII-374C13 of chromosome I, complete
                                                                                         /note-"Charlie2 repeat: matches 3272. .3479 of consensus" 54009. / 54235 / 54009. / force-"Charlie2 repeat: matches 2889. .711/ ct consensus" 56236. .57009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission

Direct Submission

Cambridgeshire, CB10 1SA, UK. F.mail enquiries:

Cambridgeshire, CB10 1SA, UK. F.mail enquiries:

Numquery@sanger.ac.uk Clone requests: clonerequest. Rsanger.ac.uk

On Jun 13, 2002 this sequence version replaced al:2126:816.

On Jun 13, 2002 this sequence vorsion replaced al:2126:816.

On Jun 13, 2002 this sequence assembly data is compared from coverlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone same. Note that the variation annotation may not be found in the sequence submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141273)
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Best Local Similarity 100.0%; Pred, No. 6.38-21;
Matches 58; Conservative 0; Mismatches 3; LoaPis
                                                                                                                                                                                                                                                                                   /note="LIMD repeat: matches 738. 64021 //note="LIMD repeat: matches 984. complement(64074. 64543)
                                                                                                                                                                                                                                                                                                                                           complement(640)4. (64543)
/note="match: GSS: Em:AQ885350"
complement(66096. (66577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(76094, .76635)
/note="match: GSS: Em:AQ277578"
complement(76184, .76636)
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complement(88581. .89052)
                                                                                                                                                                                                                                                                                                                                                                                                     /note="match: GSS: Em:AQ611651"
69990. .70342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="match: GSS: Em:A0812553"
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44071. .44491
/note="match: GSS: Em:AQ112832"
                                                       note-"match: GSS: Em:AJ247033"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"match: STS: Em:G21603"
                                     complement (45407
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AL611933.30 GI:21425229
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AL611933/C
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL: Sw.; SWISSPRYT TT. TREMEL; WPP.; WORMPEP; Information on the WORMPEP database can be found at the polyworm per this sequence was generated from part of bacterial cone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome I Mapping group. Further information can be found at
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Unpublished
Spases 1 to 145264)
Spiren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B.,
Anderson, S., Barna, N., Bastlen, V., Chang, J., Chazaro, B.,
Choepel, Y., Colandalo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., Lobarellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreita, P., FitzHugh, M., Gapen, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, M.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., LaRoque, K., Lamazares, R.,
Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M.,
McDan, P., Murphy, I., Naylor, J., Wayyen, C., Nicol, R., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Cliver, J.,
Petcrson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C.,
Retta, R., Riebark, M., Riley, R., Rise, C., Rogov, P., Roman, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/HGP/Chrl
RP11-374Cl3 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo. 1 (bases 1 to 0.145244)
Birren.H.; Linton,L.; Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-4809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC107939 145264 bp DNA linear PRI 31-MAR-1
Homo sapiens chromusome 11, clone RPII-4809, Complete sequence.
AC107939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4256 CTGCCCACCTTG3CCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACGCCCAGC 4199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1187 CTGUCGAGCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGGCCAGGC 1244
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100.0%; Pred. No. 6.5e-21;
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32122 c 33734 g 40066 t
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AC107939/C
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Location/Qualifiers Location/Qualifiers Adyzvef "taxon 9606" Colones "RP11 - 4809" Colon	/rpt_family="AluJo" 60466122 /rpt_family="1.2" 62646550 /rpt_family="AluSx" complement(6566680) /rpt_family="MERSA" complement(66816986) /rpt_family="MERSA" complement(66817057) /rpt_family="MERSA" complement(66817057) /rpt_family="MERSA" /rpt_family="LiM467635) /rpt_amily="LiM46" /rpt_amily="LiM4"	8445. 8517 8545. 8518. 8584 //pt. lamily "LIM4" 8586. 9631 //pt. lamily "LIM4" 8878. 9031 //pt. family "LIM4" 8978. 9031 //pt. family "FLAMA" //pt. family "LIM5" //pt. family "LIM5" //pt. family "MIR" //pt. family "LIM5 //pt. family "LIM5 //pt. family "MIR" //pt. family "MIR" //pt. family "Aluso" //pt. family "Aluso"
repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region	repeat_region
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TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL COMMENT

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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                   Center project name: 13990

Center clone name: 12_E_12

Sequencing vector: M13; M7815; 3% of reads
Sequencing vector: M13; M7815; 3% of reads
Sequencing vector: M3; M7815; 3% of reads
Sequencing vector: M3; M7815; 3% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 144014 bases at least Q4C
Consensus quality: 144014 bases at least Q3C
Consensus quality: 144014 bases at least Q3C
Consensus quality: 144014 bases at least Q3C
Outlity coverage: 9.4 in Q2C bases; agarose-fp
Outlity coverage: 8.3 in Q2C bases; agarose-fp
This is a "orking draft' sequence. It currently
consists of 12 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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1733 1832: gap of 100 bp
1833 2945: contig of 113 bp in length
1843 2945: contig of 1113 bp in length
2846 3045: gap of 100 bp
3046 4116: contig of 1071 bp in length
4117 4216: gap of 100 bp
4217 5757: contig of 1841 bp in length
4217 5757: contig of 1848 bp in length
5758 5857: gap of 100 bp
5858 7545: contig of 1888 bp in length
7546 7645: gap of 100 bp
11528 11527: contig of 3882 bp in length
11528 11527: contig of 3882 bp in length
11528 11527: contig of 43850 bp in length
55478 5557: gap of 100 bp
55578 6567: gap of 1100 bp
66868 6865: gap of 11106 bp in length
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8874 84073: gap of 11106 bp in length
167175 10724: gap of 100 bp
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167175 10724: gap of 100 bp
167175 107275: contig of 3101 bp in length
                                              Center code: W1BR
Web site: http://www.seq.wi.mit.edu
Web site: http://www.seq.wi.mit.edu
contact: sequence_submissions@genome.wi.mit.edu
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137396 137495: qap of 100 bp
137496 146312: contig of 8817 bp in length.
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1. 146312 ....... sabiens
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/clone-RPI:-21E12"
/clone_lib-"RPCI-11 Human Male BAC"
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/note="assembly_fragment"
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55578. .66767
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Mono sapiens clone RP11-21E12, WORKING DRAFT SEGUENCE, 12 unordered
pieces:
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia: Eutheria; Primates; Catarrhini; Hominidue; Homo.
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Unpublished
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complement(14677, 14813)
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complement(16631
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AC015494.6 GI:14209771
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Birren, B., Linton, E., Nusbaum, C. and Lander, E. Homo sapiens, clone RPil-21E14
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Contact: sequence_submissions@genome.w: mit.edu
------- Project Information
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NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                sum-of-contigs
                                                                                                      Quality coverage: 4.4 in Q20 bases; agarose-fp Quality coverage: 4.4 in Q20 bases; sum-of-cont
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154009: contig of 33818 bp in length
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Location/Qualifiers
Consensus quality: 147683 bases at least Q40 Consensus quality: 151981 bases at least Q30 Consensus quality: 153418 bases at least Q20 Inscrt size: 156000: agarose-fp Insert size: 154782: sum-of-contigs
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2. (Dases I to 158071)

8 Birron, B., Linton, L., Nusbaum, C., Lander, E., Abrahan, H., Alien, N., Anderson, S., Baldwin, J., Barnan, N., Beckelly, S., Bedd, S., Bedd, S., Baldwin, J., Barnan, B., Brekelly, S., Bedd, S., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, F., DeArellano, K., Downton, M., Doyle, M., Berestor, J., Ferretra, P., FitzHugh, W., Forrest, C., Gage, D., Galadan, J., Ferretra, P., FitzHugh, W., Forrest, C., Gage, D., Galadan, J., Landers, T., Lehoczky, J., Lewins, L., Horton, L., Marquis, N., McEwan, P., McGaran, K., McKernan, K., Meddrim, J., McMers, C., Marquis, M., McEwan, P., McGaran, K., Pierre, W., Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, D., Stolano, S., Spencer, M., Stolano, S., Stolano, J., Stolano
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Research, Linton.L., Nusbauc.C., Landet.E., All.A., Allen.N.,
Roderson, S., Barna, N., Bastlen, V., Hoom.T., Hogisslavky.L.,
Buckhgalter, B., Brown, A., Camarata, J., Campopiaton, Chans, J.,
Chazaro, B., Chopel, M., Colangelo, M., Collins, S., Collymore, A.,
Cook, P., Cooke, P., Deartellano, K., Gord, S., Geyette, M., Gradan, J.,
Faro, S., Ferreira, P., Fizzderuld, M., Fitzduqh, W., Illav, M.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Geyette, M., Uraban, L.,
Johnson, R., Jones, C., Kanata, A., Katatas, A., Kells, C., Lakorque, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., MacMan, P., Minghy, T., Naylor, C., Muphy, T., Naylor, C.,
Nicol, R., Norbu, C., Norman, C., H., Cedindor, I., Phurkhang, P., Phurken, N.,
Pollara, V., Raymond, C., Retta, R., Riese, K., Keise, C.,
Schupback, R., Sedanen, S., Seberey, P., Spencer, B., Stanger Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talanas, J., Tesfaye, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC018988 17-JUN-2002 Homo sapiens chromosome 15 clone HP11 233CT3 map 15, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
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/note-"assembly_fragment.
clone_end:T7
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ACUSBUB2 HIG 04-JJN-2000 BNA linear HTG 04-JJN-2000 HOMO Sapiens chromosome 2 clone RP11-21M2 map 2, WORKING DRAFT PROBENCE, 23 unordered pieces.
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Theodore, J., Topham, K., Travers, M., Travis, N., Trigillio, J., Vassilliev, H., Viel, R., Vo.A., Wilson, B., Mu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 1, 2002 this sequence version replaced gi:20331004.

All repeats were identified using RepeatMasker:

Smit, A.F. A. & Green, P. (1996-1997)

http://ttp-qenome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Barna, N., Bastlen, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Astlen, Y., Beda, F., Boukhalter, B. Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
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1 (bases 1 to 158450)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 2, clone RPII-21M2
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are represented as runs of N. The order of the pieces
is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently
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Project Information
Center project name: L5451
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/db_xref="taxon:9606"
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00.0%; Pred. No.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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42265: contig of 5757 bp in length
42266 42365: gap of
47307: contig of 4942 bp in length
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52538: gap of
6035: contig of 7497 bp in length
6035: gap of
6035: contig of 8442 bp in length
68457 68456: gap of
76899 68527: contig of 8442 bp in length
76899 68527: contig of 8429 bp in length
76899 68527: contig of 100 bp
7699 68528 65927: gap of
7699 68528: gap of
7699 68527: contig of 100 bp
7699 100028: gap of
7699 11274: contig of 12501 bp in length
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7699 11277: contig of 12513 bp in length
7698 11277: contig of 100 bp
7698 11277: contig of 100 bp
7698 112878: contig of 100 bp
7698 112878: contig of 100 bp
7698 11387: gap of
7698 11387: contig of 17063 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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68457. 76698
/note assembly_fragment*
7699. 85827
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1850, 3169
/note-"assembly_fragment"
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/note="assembly_fragment"
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/note-"assembly_fragment"
8098. 13045
/note="assembly_fragment"
13146. 16766
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/db_xref-"taxon:9606"
/chromosome-"2"
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                        Galagan, J. Gardyna, S., Gardyna, S., Goyette, M., Gardyna, S., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Landers, T., Karun, L., Karquis, R., Lewine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGarthy, M., McBwan, P., McGrick, A., McGarthy, M., McBwan, P., McGrick, A., Mardyna, J., Marcha, C., McGrick, M., McGrick, McGrick, McGrick, McGrick, McGrick, McGrick, McGrick, McGrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contins are represented as runs of N, but the exact sizes of the days are represented as fins econd will be updated with the traissed sequence as soon as it is available and the tensestes, uncher will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 163000; agarose-tp
Insert size: 156250; sum-of-cont.iqs
Quality Coverage: 3.6 in 020 bases: agar.se-tp
Quality coverage: 3.8 in 020 bases: sum-of-cont.iqs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center close name: 21.M_2

Center close name: 21.M_2

Sequencing vector: M13: M77815; 100% or reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap: version 0.9607:1

Consensus quality: 146955 bases at least Q40

Consensus quality: 155308 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_summiss!cons@gencme.wi.rit.edu
Center project Information
Center project name: L10095
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23844 27652: contig of 3809 bp in length
27653 27752: gap of 100 bp
27753 31395: contig of 3843 bp in engith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13046 13145: gap of 100 bp
13146 16766: contig of 3621 bp in length
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23743: contig of 2784 bp in length
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         Domino, M., Doyle, M., Ferreira, P.,
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27753 31395; cont.)
31396 31495; gap of
31496 36409 of
36409 36508; gap of
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20859: con
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COMMENT

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Homo sapiens chromosome 2 clone RP11-21M2, WYRKING DRAFT SEQUENCE.
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Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Fark Farkway, St. Louis,
MO 61108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae: Homo.
1 (bases 1 to 162419)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                       UP 64666 CTGCCCACCTTGGCCTCCCAAAGTGCTGGATTACAGGATGAGGCACTGAGGCAAGTGCGAGG 64009
                                                                                                                                                                                                                                                                                                      Saps
                                                                                                                                                                                                                                                                                                                                              QY 1187 CIGGCCACCTTGGCCTCCCAAAGTGGGATTACAGGGATGAGAAAGTGCGAGG 1244

    arbitrary. Gaps between the contigs are represented as

            runs of N, but the exact sizes of the gaps are unknown.
            This record will be updated with the finished sequence
            as soon as it is available and the accession number will
            be preserved.

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                                                                                                                                                                                                                                                  Length 158450;
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                                                                                                                                                                               2204 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/qsc/index.shtsd
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HTG: HTGS_PHASE1: HTGS_DRAFT: HTGS_FULLTOP
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                                                                                 The sequence of Homo sapiens clone Unpublished
              /note="assembly_fragment"
109029, 121274
/note="assembly_fragment"
121375, 141287
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96428. .108928
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Waterston, R. H.
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AUTHORS
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AC053737
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KEYWORDS
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LOCUS

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Db 52046 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 52103
                                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Pred, No. 6.6e-21;
Live 0: Mismatches 0;
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: 30933 c 30950 g 50417 t
                                 /organism."Homo sapiens"
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Best Local Similarity 100.0
Matches 58; Conservative
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5 PCT-0595-07201-43 Sequence 43, Appl 4 US-09-875-223-2 Sequence 2, Appl 4 US-09-797-906-3 Sequence 3, Appl 2 US-08-724-394A-20 Sequence 20, Appl	US-08-724-394A-21	US-09-374-454-20 Sequence 20, US-09-741-150-3 Sequence 3,	US-09-128-135-1/ Sequence 17, US-08-471-570-9 Sequence 9, US-08-471-570-9	US-08-4/1-5/0-/ Sequence /, US-08-975-080-35 Sequence 35,	US-09-630-706-10 Sequence 10, IIS-09-496-6948-3	US-09-341-587-7 Sequence 7,	US-09-780-049-18 Sequence 18, US-09-851-896-3	US-09-268-992-7 Sequence 7,	US-09-657-474-7 Sequence 7,	US-09-73U-38U-1 Sequence 1, US-09-791-211-10 Sequence 10,	US-09-798-096-10 Sequence 10,	US-08-324-465-2 Sequence 1, US-08-324-465-2	US-08-465-981-2 Sequence 2,	PC1-0593-11915-2 Sequence 2, US-08-324-465-5 Sequence 5.	US-08-465-981-5 Sequence 5,	PCT-US93-11915-5 Sequence 5, US-DR-655-640-5 Sequence 5	US-09-050-159-129 Sequence 129	US-09-800-960-3 US-08-967-101-107 Saguence 107	US-08-592-541-107 Sequence 107	US-09-124-698-107 Sequence 10	US-09-12/-400-10/ US-08-496-841C-107 Sequence 10	US-09-124-523-107 Sequence 10	US-08-967-101-103 Sequence 1 US-08-592-541-103 Sequence	US-09-124-698-103 Sequence 10	US-09-127-480-103 Sequence 10 US-08-496-841C-103 Sequence 10	US-09-124-523-103 Sequence 10	US-09-227-357-74 Sequence 74	US-08-592-541-13 Sequence 13	US-09-124-698-13 Sequence 13	US-U9-12/-480-13 Sequence 1: US-08-496-8410-13 Sequence 1:	US-09-124-523-13 Sequence 1	US-08-943-731-31 Seguence 31	US-08-967-101-156 Sequence 15	113-08-888-0278-6	US-09-124-698-156 Sequence 15	US-09-127-480-156 Sequence 15	US-08-496-84IC-156 Sequence 15	US-08-852-807-10 Sequence 10	US-08-886-152-4 Sequence 4,	US-09-196-222-4 Sequence 4,	US-09-0/8-294-/ Sequence /, US-08-852-807-1 Sequence 1,	US-08-943-731-1 Sequence 1,	US-08-310-356-36 Sequence 36	PCT-US92-06300-1 Sequence 1.	US-08-814-095-7 Sequence 7,	US-09-734-073-3 US-09-791-211-10 Segmence 10	US-09-798-096-10 Sequence 10	US-09-426-290-1 Sequence 1,
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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen ::3.	rucleic search, using sw model	ond	pdat	US-09-846-456-3	Coccaso to the total of the tot		OLIGO_NUC Gabop 60.0 . Gapext 60.0		441362 segs, 153338381 residues		7	restring chosen parameters.	Seq Tength: 0	2000000000	: Listing first 1000 summaries	ued Patents NA:*	/cgn2_6/ptodata/1/ina/5A_COMB.seq:*	: /cgnz_b/ptodata/l/lba/bB_cCMB.seq:* : /cgn2_6/ptodata/l/lba/6A_COMB.seq:*	/cgn2_6/ptodata/1/ina/68_COMB.seq:*	/cqn2_6/ptodata/1/ina/PCTUS_COMB.seq:* /cqn2_6/ptodata/1/ina/backfiles1_seq:*	/ CGITZ_C/ PCOCACA/ 1/ 1114/ CGC/ 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	chance to have a	print		SUMMARTES		DB ID	246240 2 US-08-724-394A-20 sequence 20	246240 2 US-08-724-394A-21 Sequence 21	240240 Z 03.00-724 4948 ZZ SCHIEDGE ZZ 162450 4 (IS-09-345 842 )	162450 4 US-09-345-882-1 Sequence :.	866 4 US-09-257-179-11 Sequence 11	21234 4 US-09-810-671-3 Sequence 3.	31571 1 US-08-323-443B : Sequence 1.	36651 4 US-09-738-894A-3 Sequence 3,	53526 3 US-08-658-136-2 Sequence 2,	335// 3 US-08-68-136-1 13158 2 US-08-687-080-105 Sequence 10	153 2 US-08-849-701-2 Sequence 2,	891 4 US-09-247-155-141 Sequence 14	1701 4 US-09-288-143-16 Sequence 16	. 7	3267 4 US-08-367-841A-12 Sequence 12	3267 5 PCT-US95-07201-12 sequence 12	3663 4 US-09-499-884-11 Sequence 11	3844 4 US-09-689-423-1 Sequence 1. 5262 4 US-08-520-3730-5	5581 4 US-08-973-544-1 Sequence 3.	8396 4 US-09-328-174A-1 Sequence 1,	8409 4 US-09-167-681-37 Sequence 37

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US-09-227-357-92 US-09-16-322-14 US-09-16-322-14 US-09-16-322-14 US-09-16-322-14 US-09-734-675-3 US-09-734-675-3 US-09-734-675-3 US-09-734-675-3 US-09-734-675-3 US-09-734-675-3 US-09-734-14-6 US-09-734-14-6 US-09-736-344-1 US-09-736-344-1 US-09-736-344-1 US-09-736-344-1 US-09-736-344-1 US-09-128-155-16-1 US-09-128-15-16-1 US-09-128-15-16-1 US-09-128-15-16-1 US-09-128-11-1 US-08-128-11-1 US-08-138-11-1 US-08-138-14-1 US-08-138-14-1 US-08-138-14-1 US-08-138-14-1 US-08-14-11-1 US-08-14-11-1 US-08-14-11-1 US-08-14-11-1 US-08-14-11-1 US-08-14-11-1 US-08-14-11-1 US-08-14-11-1 US-08-14-11-1 US-08-14-1-1 US-08-14-1-1 US-08-14-1-1 US-08-14-1	
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4 US-09-375-318-36 4 US-09-026-033-17 4 US-09-130-491-5 4 US-09-130-491-5 1 US-08-18-19-19-15-19-19-19-19-19-19-19-19-19-19-19-19-19-	US-09-277-457-27 US-09-2734-60 US-08-443-731-4 US-08-978-294-6 US-09-788-894-3 ALIGNMENTS ALIGNMENTS ALIGNMENTS ALIGNMENTS Y S. Y S
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ောင်းသို့သို့လိုက်သို့ကိုကိုကို လိုင်းသည်။ လေရိုင်လိုင်းသည်။ လေလာလာလာလည်းကိုကိုကိုကို လိုင်းသည် လေရိုင်လိုကို လေလိုင်းသည်။ လေလာလာလာလည်းသည်။	Sequence 6, Appliance of Appliance 2, Applia
	0S-09-146-053+6 0S-09-746-053+6 0S-09-754-250-1 0S-09-754-250-1 0S-09-754-250-1 0S-09-754-250-1 0S-09-754-250-1 0S-09-754-250-1 0S-08-450-67-91 0S-08-450-67-91 0S-08-450-67-92 0S-08-450-67-92 0S-08-450-67-92 0S-09-385-401-45 0S-09-385-401-14 0S-09-385-401-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-257-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14 0S-09-357-171-14
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                                                                                                                                                                                                                                                                                                                                                      1.9%; Score 55; DR 2; Lorons, Pred. No. 3,5e-15;
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San Francisco
                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note- "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 3.6
Mismatches
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                                       017957-000100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/38724394A
Futent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
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NAME: FILE, REDEE A.
REJISTRATION NUMBER: 35,186
REFERENCE/DOCKEI NUMBER: 0179;
NELECOMNUNICATION INFORMATION:
TELEDHONE: 415-576-0200
FELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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not relevant
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                                                                                               TELEFAX: 415-576-0300
INFURMATION FOR SEQ ID NO: 20:
                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
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                                                                                           415-576-0300
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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STRANDEDNESS: not r
                                                                                                                                                                         nucleic acid
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Matches 55; Conserva
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US U8-724-394A-21/c
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Gaps
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                                                                                                                                                                                          Db 14447 CCCACCTTGCCAAAGTGCTGGAATTACAGGCATGAGCCACTGGGCCCAG 14393
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                                                                                                        Length 246240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e; IITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLIFATION DATA:
                                                                                                      Ouery Match 1.9%; Score 55; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 3.6e-15;
Matches 55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE AUDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.9%; Score 55; DB 2; Lv 100.0%; Pred. No. 3.6e-15; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Two Embarcadero Center, 8th Floor
San Francisco
NAME/KEY: misc_teature
COCATION: 1..246240
COCATION: A..246240
US-08-724-5948-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note- "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Filts, Kenee A. REGISTRATION NEMBER: 15,136
REGISTRATION NEMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEFHONE: 415-576-0200
TELEFAX: 415-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/724, 394A FILING DATE: 0:-0:-0:-1:996 CLASSIFICATION: 536 AFFORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                ; Sequence 22, Application US/08724394A; Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas, Winston
APPLICANT: Isuchibashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Feder, John N. APPLICANT: Kronmal, Gregory S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SS: not relevant not relevant
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INFORMATION FOR SEQ ID NO: 22:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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LOCATION: 1..246240
OTHER INFORMATION: /not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: not r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 55; Conserv
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94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                            US-08-724-394A-22/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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OTHER INFORMATION: polymorphic tragment 99-1442-224 SEQ ID50
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                                                                                                                   OTHER INFORMATION: 5-136-174 FEATURE:
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OTHER INFORMATION: 5-148-352
ON: 108308
INFORMATION: 5-135-357
                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: 5-140-348
                                                                                                                                                                                                                         5-140-120
                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: 5-140-361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 5-143-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ION: 146328
INFORMATION: 5-143-84
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Patent No. 6399373
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OTHEK INFORMATION: 5-128-60 :
FEATURE:
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OTHER INFORMATION: 99-1437-325
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LOCATION: 97122
OTHER INFORMATION: 99-1442-224
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LOCATION: 108149
OTHER INFORMATION: 5-135-198
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LUCATION: 88073
OTHER INFORMATION: 5-127-261
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OTHER INFORMATION: 5-133-375
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LOCATION: 99098
OTHER INFORMATION: 5-130-257
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OTHER INFORMATION: 5-130-276
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CTHER INFORMATION: 5-131-395
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OTHER INFORMATION:
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LOCATION: 97152
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LOCATION: 99117
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LOCATION: 90819...90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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LOCATION: 72771...72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
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LOCATION: 880590..88096
OTHER INFORMATION: polymorphic tragment 5-127-261 SEQ ID52
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OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID33
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OTHER INFORMATION: POLymorphic fragment 5-128-60 SEQ ID32
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APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTCMA BINDING PROTEIN (
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/05/345,882
CURRENT APPLICATION NUMBER: US/05/345,882
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06 30
PRIOR FILING DATE: 1998-12-10
NUMBER OF SED 10 NOS: 140
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LOCATION: 108471
OTHER INFORMATION: 5
FEATURE:
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LOCATION: 106940
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 88073
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LOCATION: 72794
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Pred. No. 2:1e 13:
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       OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ :1971
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LOCATION: 108127...108177
LOCATION: 108127...108177
FORTHER INFORMATION: polymorphic fragment 5-135-198 SEQ :11-3-
FORTHURE:
NAME/KEY: allele
LOCATION: 108127...108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ :11-6
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                                                    NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEO
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LOCATION: 97130..97177
OTHER INFORMATION: polymotphic fragment 5-129-144 SEQ
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LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5:133-375 SEQ
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LOCALION: 99094..99140
OTHER INFORMATION: Polymorphic tragment 5-130-276
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OTHER INFORMATION: polymorphic fragment 5-131-335
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LOCATION: 103783..103828
UTHER INFORMATION: polymorphic fragment 5:13)
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US-09-445-882-1/c
Sequence 1, Application US/09345882
Patent No. 639933
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 51, Conservative
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LCCATION: 108084..108130
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LOCATION: 99094..99140
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LOCATION: 99075..99121
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LOCATION: 99075.,99121
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LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ HTM
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LOCATION: 97099, 97145
OTHER INFORMATION: Polymorphic fragment 99-1442 224 SEG
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LOCATION: 72771..72817
VYHEK INFORMATION: polymorphic fragment. 5-124-273 SEO
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OTHER INFORMATION: polymorphic tragment 5 128-60
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LOCATION: 88050..88096
CTHER INFORMATION: polymorphic fragment 5-12?
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LOCATION: 93690..93736
CTHER INFORMATION: polymorphic tragment, 5-128
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OTHER INFORMATION: 5-148-352
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LOCATION: 90819..90865
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NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCALION: 150329
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LOCATION: 108127..108177
OTHER INFORMATION: FOlymorphic fragment 5-135-198 SEQ ID60
                                                                                               LOCATION: 99075...99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: polymorphic tragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: polymorphic fragment 5-135-155 SEQ 1D59
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ON: 97130...97177
INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
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OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5-135-155 SEQ
                                                                                                                                                                    NAME/KEY: allele
LOCATION: 99075, 99121
OTHER INFORMATION: polymorphic fragment 5-130-257
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100.0%; Pred. No. 6e-13;
1ve 0; Mismatches 0;
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IIILE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CORRENT APPLICATION NUMBER: US/09/257,179
CORRENT FILING PAIE: 1999-02-25
EARLIER APPLICATION NUMBER: PCT/US98/17709
EARLIER FILING DAIE: 1998-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 108084...108130
OTHER INFORMATION: polymorphic fragment
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Patent No. 6410709
GENERAL INFORMATION:
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LOCATION: 106918..106966
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LOCATION: 108084..108130
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LOCATION: 106918..106966
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ORGANISM: Human
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                                                                             SEQ ID NO 3
LENGTH: 36159
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APPLICANT:
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                                                                                                                              IYPE: DNA
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APPLICANT: YAN, Chunhua et al
APPLICANT: YAN, Chunhua et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE FRITEINS, NUCLEUP
TITLE OF INVENTION: ACID MOLECULES ENCUDING HUMAN KINASE PROFINIS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOUTS8
CURKENT PAPLICATION NUMBER: US/09/RIG.67)
CORRENT FILING DATE: 2001-06-08
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SOFTWARE: PastSEQ for Windows Version 4 D
EARLIER APPLICATION NUMBER: 66/056,270
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 66/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,247
EARLIER APPLICATION NUMBER: 60/056,013
EARLIER APPLICATION NUMBER: 60/056,073
EARLIER FILING DATE: 1997-08-29
EARLIER FILING DATE: 1997-08-29
NUMBER OF SEQ ID NOS: 128
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COTHER INFORMATION: n equals a,t,g, or c
US-09-257-179-11
                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (22)
OTHER INFORMATION: n equals a,t,g, or
FEATURE:
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Patent No. 6455291
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Rest Local Similarity 100.0
Marches 49; Conservative
                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                             CKGANISM: Homo sapiens
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US-09-810-671 3
                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
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LENGTH: 866
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                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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Caps
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                                                                                                                                                                                                                                                                           1.7%; Score 49; DB 4; Length 361
100.0%; Pred. No. 1.8e-12;
Live 0: Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: POLYCYSTIC KILNEY DISEASE GENE NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/22,4448 FILING DATE: 12-007-1994
CURRENT FILLING DATE: 2000-12-28
NUMBER OF SEQ 15 NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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12.00TH: 1994
N: 435
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM IYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC:00S/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // Sequence 1, Application US/08323443B
// Patent No. 5654170
                                                                                                                                                                   NAME/KEY: misc_lealure
LCCATION: (1)...(*6159)
OTHER INFORMATION: n + A,T,C or G
US:09-749-5888-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KLINGER, KATHERINE W. APPLICANT: LANDES, GREGORY M. APPLICANT: HURN, TIMCTHY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: CONNORS, TIMOTHY D. APPLICANT: DACKOWSKI, WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dathy & Darby PC STREET: 805 Third Avenue
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REGISTRATION NUMBER: 25,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GERMINO, GREGORY
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LENGTH: 31571 base pairs
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Best Local Similarity 100.(
Matches 49; Conservative
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IMMEDIATE SCHLOF.
CLONE: PKOL GENOMIT
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10022
PF
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us-09-846-456-3.oli30.rni

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Gaps
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Pred. No. 4.8e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                     1712 CTGCCCACCTTGCCTCCCAAAGTGCTGGGATTACAGGCATGAGGCCAC 1759
                                                                                                                                                                                                                                                                                                                                                                             1187 CIGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 1234
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
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100.0%; Pred. No. 4.8e-12;
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Best Local Similarity 100.0%: Pred. No. 4.84
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                                           GEN4 17.8
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MEDIUM TYPE: Fioppy disk
COMPUTER: IN FC Compatible
OPERATING SYSTEM: PC-FOS/MS DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BLEN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/U8658136
Patent No. 6071717
                        31,845
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GERMIND, GREGORY
                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 508:872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOORSET NUMBER: GRIELECOMMUNICALION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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                                                                                                TELEFAX: 508-8/2-5415
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACLERISTICS:
LENGTH: 5/3526 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 53577 base pairs
                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508-872-8400
  LASSEN, ELIZABETH
                                                                 TECEPHONE: 508 0.2

TECEPHONE: 508 872-5415

""" ""AX; 508-872-5415
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                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sinale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 508 872-5415
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASSACHUSETTS
                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PO NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OIAN, FENG
                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                       Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAM I NGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01701
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APPLICANT:
                                                                                                                                                                                                                                                              US-08-658-136-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
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                                                                                                                                                                                                           Sequence 3, Application US/09738894A
Patent No. 6331423
SENERAL INFORMATION
SENERAL INFORMATION: SOLATED HUMAN KINASE PROTEINS, NUCLEST
TILLE OF INVENTION: ACID MOLECULES ENCOSING HUMAN KINASE (ROTEINS, AND USES)
TILLE OF INVENTION: THEREOF
FILE REFERENCE: CLUO0656
CURRENT APPLICATION NUMBER: US/09/738,894A
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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  DB 1; Length 31571;
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                                                                                                    1187 CTGGCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGGGAG 1234
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                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: KLINGER, KATHERINE W
APPLICANT: CONNORS, TROOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DCKNORSI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: GERMINO, GREGORY
APPLICANT: OLAN, FENG
APPLICANT: OLAN, FENG
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-NOS
SOFTWARE: Patentin Release #1.0. Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 1.7%; Score 48; BB 4; Lea
Best Local Similarity 100.0%; Pred. No. 4.9e-12;
Matches 48; Conservative 0; Mismatches 0;
1.7%; Score 48; DB 1; LA
100.0%; Pred. No. 4.9e-12;
          100.0%; Pred. nv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENZYME CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
Location: (i)...(36651)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08658136
Patent No. 6071717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: ONE MOUNTAIN ROAD CITY: FRAMINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALFORNEY/AGENT INFORMATION
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MASSACHUSETTS: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                            US 09-718-894A-3/C
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US 08-658 136-2
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  Overy Match
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CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe, Martens, Olson & Bear
STREET: 620 Newport. Center Drive 16th Floor
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                                                                                                                                                             COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                       714-760-0404
                                                                                                                                                                                                                                                                                                                                                                  NAME: Altman, Daniel E
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 153 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                              Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 714-760-04
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
                                                                                                                       COMPUTER READABLE FORM:
                                                       Newport Beach
                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Home sapiens
                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                       U.S.A.
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US-09-247-155-141/c
                                                                                                                                          MEDIUM TYPE:
                                                                                                        92660
                                                                        STATE: CA
                                                                                                                                                                                                     SOFTWARE:
                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-849-701-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
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                                                                                                                                                                                                 APPLICANT: Gregory Dolganov
TITLE OF INVENTION: Human RADSG Gene and Methods of Use Thereof
NUMBER OF SEQUENCES: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.6%; Score 47; DB 2; Lenath 1:58
100.0%; Pred. No. 1.4e-11;
                                    1187 CIGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGGCAC 1234
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 17-JUL-1996
CLASSIFICATION: 435
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APPLICANT: Maitob, Tsutomu
APPLICANT: Yonekawa, Toshihiro
TILE OF INVENTION: Method of Cell Detection
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. nc.
                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 175
CORRESPONDENTE ADDRESS:
AUDRESSEE: Debiinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4600 .01:11. 10
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                                                                                                                                            Sequence 195, Application US/08687080 Patent No. 5965427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08849701; Patent No. 5922544; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Sholtz, Charles K.
REGISIRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION: FELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38,615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 13158 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuery Match
Hest Local Similarity 100.Uv
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                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             Palo Alto
                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                           STATE: CA
COUNTRY: USE
ZIP: 94306
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                                                                                                          RESULT 13
US:08-687-080-105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CCCACCTTGGCCCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.6%; Score 45; DB 2; Lo
100.0%; Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, Jean-Baptiste
APPLICANT: Duckert, Aymeric
APPLICANT: Bouqueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.55
Best Local Similarity 100.0%; Mismatches
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CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
FARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
EARLIER FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: EIKENI,001APC TELECOMMUNICATION:
                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02734
FILING DATE: 27-DEC-1995
ATTORNEY/AGENT INFORMATION:
                                             CURKENT APPLICATION DATA: APPLICATION NUMBER: US/08/849,701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 141, Application US/09247155A Patent No. 6312922
SYSTEM: DOS
FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                     34,115
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Gaps

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APPLICANT: PALICIA SCHWAITZ, JOAN P.;
APPLICANT: PALICIA SCHWAITZ, JOAN P.;
TITLE OF INVENTION: PIGMENT EPITHELINE TITLE OF INVENTION: PIGMENTED FACTOR: CHARACTERIZATION OF ITS NOVEL.
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL.
TITLE OF INVENTION: ALOUGH ACTIVITY AND SEQUENCES ENCOSING
TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1033 AACCICTGCCTGCCGGGTTCAAGGGATTCTCCTGCCTCAGCCTCC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1182 AACCTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCC 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match i.6%; Score 45; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 45; Consorvative 0; Mismatches 0;
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLETC ACID MOLECULE
FILE REFERENCE: Davies Col
CURRENT APPLICATION NUMBER: US/09/078,294
FURRENT FILING DATE: 1998-05-13
NUMBER OF SEC 1D NGS: 29
SOFTWARE: Patcntin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chader, Gerald J.; Becerra, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION METHOD:
OTHER INFORMATION: 3.3 Kb PCK product.
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REFERENCE/CACKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38/08/257, 963B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDICM TYPE: Floppy Disk
COMPUTER: HM PC Compatible
COMPATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: W-MSDEREECT 5.1
CURRENT APPLICATION DATA: AS/C8/257,96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08257963B
Patent No. 5840686
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APPLICATION NUMBER: 07/952,796
FILING DALE: 24-SEPT 1992
ATTORNEY/AGEN? INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Morgan & Finnegan
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 758-4800 TELEFAX: (212) 751 6849 INFORMATION FOR SEQ 1D NC: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genomic DNA
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                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: BAC F2 conting 5
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acid
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
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STREET: 345
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US-08-257-9638-12
                                                                                                                                                                                                                                                                            LENGIH: 1701
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STATE:
                                                                                                                                                                                                                                        SEQ ID NO 9
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100.0%; Pred. No. 1.20-10;
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five 0; Mismatches
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CURKENT FILING DATE: 1999-04-08
EARLIER APPLICATION NUMBER: PCT/US98/21142
FARLIER FILING DATE: 1998-10-08
EARLIER FILING DATE: 1998-10-09
EARLIER FILING DATE: 1997-10-09
FARLIER APPLICATION NUMBER: 60/061,529
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER APPLICATION NUMBER: 60/061,529
EARLIER APPLICATION NUMBER: 60/061,548
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                                                                                                                                                                  OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: Score 5.6999980926514
OTHER INFORMATION: Seq LLLFFGKILVVGG/VG
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00.0%; Pred. No.
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EARLIER APPLICATION UNBER: 60/661,527
EARLIER APPLICATION UNBER: 60/661,527
EARLIER APPLICATION NUMBER: 60/661,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: 60/061,532
EARLIER FILING DATE: 1997-10-09
NUMBER: DESQ ID NOS: 219
SOFTWARE: Patentin Ver. 2.0
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Fatent No. 6433139
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US-09 078-294-9
IS-09 078-294-9
Sequence 9, Application US/09078294
Patent No. 6265211
GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 45; Conservative
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Best Local Similarity 100.0
Matches 45; Conservative
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APPLICANT: Brower et al.
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                                                                                                                                                                                                                                                                                                        NAME/KEY: polyA_signal
LOCATION: 858..863
                                                                                               NAME/KEY: Siq_peptide
LOCATION: 4..147
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: POLYA_Site
LOCATION: 880..891
09:247-155-141
                                      COCATION: 4..447
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   NAME/KEY: CDS
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us-09-846-456-3.oli30.rni

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APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Particia: Schwartz, Joan P.;
APPLICANT: Particia: Schwartz, Joan P.;
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DEKIVED FACTOR: CHARACTERIZATION GENOM!C
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SECUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: 3.3 kb PCR product OTHER INFORMATION: using primers, SEQ ID No: 15 and 16
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613 CCCACCITGGCCTCCCAAAGTGCTGGGATTACAGGCATGACCAC 657
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    Morgan & Finnegan, L.L.P.
    Park Avenue

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                                                                                                                             Sequence 12, Application PC/10S9507201 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/557 764
FILING ARM
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APPLICATION NINHER: 08/357,841
FILING DATE: 30-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: DORUTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DYCKET NUMBER: 20
TELECOMMUNICATION INFOHMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 758-4860
(212) 751-6849
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AITORNEY/AGENT INFORMATION:
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LENGTH: 3267 Hase Pairs
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CITY: New York
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                                                                                     RESULT 20
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CTHER INFORMATION: using primers, SEQ ID No. 5319687 [5 and 16 US:08-367-841A-12
using primers, SEQ ID No. 5840686 15 and 16
                                                                                                                                                                                                                                                                                                                                                                                                                                PIGMENT PETTHELIUM
DERIVED FACTOR: CHARACTERIZATION GENERAL
ORGANIZATION AND SEQUENCE OF THE PEDE GENE
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                                                              1.6%; Score 45; DB 2; Length 3277; 100.0%; Pred. No. 1.20-10;
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100.0%; Pred. No. 1.26-10;
Live 0; Mismatches 0; Ecdo.
                                                                                                                                                    1190 CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 1234
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                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Iombran-Tink, Joyce
                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08367841A Patent No. 6319687 GENERAL INFORMATION: APPLICANT: Chader, Gerald 3.; Rodriquez.
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REFERENCE/DOCKET NUMBER: 20264126USZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/367.841A FILLING DATE: 30-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-IX)S
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PIGMENT EPITH
TITLE OF INVENTION: DERIVED FACTO
TITLE OF INVENTION: ORGANIZATION
NUMBER OF SEQUENCES: 43
CORRESPONDINGE ADDRESS:
SIREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NOMBER: 08/257,963
FILING DATE: 07-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/952,796
FILLING DATE: 24-SEP 1992
ALTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 758-4800 TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 3267 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: Genomic DNA
                                                                                   Best Local Similarity 100.0
Matches 45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Nucleic Acid
STRANDEDNESS: Double
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PRIOR APPLICATION DATA:
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) OTHER INFORMATION:
US-08-257-963B-12
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Best Local Similarity
Thos 45; Conserva
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SIATE: New York
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                                                              Query Match
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Length 3267;

DB 5; Le 1.2e-10;

0S-09-495 884-11/c

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OTHER INFORMATION: EXON 35-161; EXON 1142-1297; EXON 1984-2187; OTHER INFORMATION: EXON 5170-5255; IMTRON 162-1141; INTRON OTHER INFORMATION: 1298-1983; INTRON 2188-5169; CDS 35-161; CDS OTHER INFORMATION: 1142-1297; CDS 1984-2187; CDS 5170-5255 NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        655 Fifteenth St., NW, Suite 300, G St. Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1190 CCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 1234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEW IMMUNOREGULATORY PROTEIN LST-1 NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
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: OTHER INFORMATION: n - a or g or t or c, any base
US-08-520-373D-5
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100.0%; Pred. No. 1.1e-10;
tive 0; Mismatches 0;
                  CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/277,710
PRIOR FILING DATE: 1995-01-25
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1994-07-25
PRIOR FILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-06-04
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ 1D N/S: 34
SOFTWARE: PALENTIN VOY: 2.1
SEQ 1D N/S
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT EP 96/02663
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; Sequence 1, Application US/08973544
; Patent No. 6338950
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APPLICANT: WEISS, Elisabeth
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COMPUTER READAHLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 100.0
Matches 45; Conservative
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NAME/KEY: exon
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ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
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GENERAL INFORMATION:

APPLICANT: S. Clair, Daret

APPLICANT: S. Clair, Daret

APPLICANT: Branch Wineyasu

APPLICANT: Rasarskis, Edward

APPLICANT: Rasarskis, Edward

APPLICANT: Rasarskis, Edward

APPLICANT: Branch Wineyasu

APPLICANT: Rasarskis, Edward

APPLICANT: Branch Wineyasu

APPLICANT: Branch Wineyasu

Title OF INVENTION: BASSOLATED DISEASES

FILE REFERENCE: 50229-180

CURRENT APPLICATION NUMBER: US/09/499, 884

CURRENT FILING DATE: 2000-02-08

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3 0
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APPLICANT: Steele, Fintan R
APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Johnson, Lincoln V
APPLICANT: Rodriguez, Ignacio R
APPLICANT: ROdriguez, Ignacio R
FILE OF INVENTION: RETINE PIGMENTED EPITHELIUM DERIVED NETROPIC FACTOR
FILE REFERENCE: 2026-4203US1
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TITLE DE INVENTION: Gene and Methods fo: Diagnosina Neuropsychiatric TITLE DE INVENTION: Gene and Treating Such Disorders
TITLE DE INVENTION: Disorders and Treating Such Disorders
FILE REFERENCE: PENN-0731
CURRENT APPLICATION NUMBER: US/09/689,423
CURRENT APPLICATION NUMBER: US/09/680, 423
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 66/159,554
PRIOR APPLICATION NUMBER: 66/159,354
PRIOR APPLICATION NUMBER: 66/159,354
NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin Ver: 2.1
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; Sequence 3, Application US/09689423
; Fatent No. 6414131
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Matches 45; Conservative
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: GRGANISM: Homo sapiens
03-09-689-423-1
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US-09-499-884-11
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LENGTH: 3663
TYPE: DNA
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TITLE OF INVENTION: PIGNEWT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
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                         Indels
                                                                                                                                                                                     Sequence 37, Application US/09167681A
Patent No. 626561
GENERAL INFORMATION:
APPLICANT: Methorishiboum, M.D., Richard M.
APPLICANT: Refroquents, Rebecca B.
APPLICANT: Modd, Thomas C.
TITLE OF INVENTION: SULFOTRANSFERASE SEQUENCE VARIANTS
FILE REFERENCE: 07039/118001
CURRENT APPLICATION NUMBER: US/09/167,681A
CURRENT FILING DATE: 1998-10-07
                                                            1033 AACCICTGCCCCCCCCCCTTCAACCGATTCTCCTGCCTCAGCCTCC 1077
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100.0%; Pred. No. 1.1e-10;
ive 0; Mismatches 0;
     100.0%; Pred. No. 1.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEU for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43, Application US/08367841A; Patent No. 6319687
GENERAL INFORMATION:
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Hest Local Simplarity 100.0%; Pr
Matches 45; Conservative 0;
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345 Park Avenue
 Best Local Similarity 100./
Matches 45; Conservative
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LOCATION: (3987)...(4112)
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LOCATION: (6369)...(6404)
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LOCATION: (7214)...(7393)
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LOCATION: (3730)...(3879)
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(4198)...(4293)
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                                                                                                      RESULT 26
US-09-167-681-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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G
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APPLICANT: Guida, Marco
APPLICANT: Guida, Marco
APPLICANT: Kurth, Janice
TITLE OF INVENTION: (STP2)
FILE REFERENCE: 4389-6 (formerly SEQ-16F)
CURRENT APPLICATION NUMBER: 08/09/328,174A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 09/328,174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
1.6%; Score 45; 58 4; Lenath 958;
Best Local Similarity 100.0%; Pred. No. 1.1e 10;
Matches 45; Conservative 0; Mismatches 3; Eddens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 85.46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APELICATION NUMBER: EP 95112201.9
APPLICATION NUMBER: EP 95112201.9
FILING DATE: 03-AUG-1995
ALTGENEY AGENI INPORMATION:
NAME: Kitts, Monited Chin
RECISTRATION NUMBER: 36,105
RECISTRATION NUMBER: 36,105
RECISTRATION NUMBER: 36,105
FELECHMUNICATION INPORMATION:
TELECHCOMMUNICATION INPORMATION:
TELECHCOMMUNICATION SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5581 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ 1D NOS: 110
SOFTWARE: FastSEQ for Windows Version 3.0
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FILING DATE: 20-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95109511.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09328174A
Patent No. 6448003
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                        FILING DATE: 20-JUN-1995
PRICH APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
2325..2709
                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
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1775..1797
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1475..1567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544..652
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; ORCANISM: H. sapiens
US 09-328-174A-1
                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                     exon
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08/367,841

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FEATURE:
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GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becetts, Soliu
APPLICANT: Patricial Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PICHEMI EPITHELLUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION J.N.MIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PETF GENE
NUMBER OF SEQUENCES: 43
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OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus llanking sequences.
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100.0%; Pred. No. 1.1e-10;
1ve 0; Mismatches 0; Indels (
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Best Local Similarity 100.0%; Pred. No. ....
Marches 45; Conservative 0; Mismatches
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                                                                                                      APPLICATION NUMBER: US/08/367,841A FILING DATE: 30-DEC-1994 CLASSIFICATION: 435
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FILING DATE: 06-JUN-1995
                                                                                                                           FILING DATE: 30-DEC-1994
CLASSIFICATION 415
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA: 07/952,796
FILING DATE: 24-SEP-1992
AITCARIOY AGGENT INFORMATION:
                  COMPUTER: 1BM PC Compatible CORFALING SYSTEM: PC-005/MS-DOS SOFTWARE: WORDPERECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFRENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk
Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22481 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Genomic DNA
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MEDIUM IYPE:
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GYBERAL NO. 69 19 10 A.
APPLICANT: No. 69 19 15 A.
APPLICANT: David Dawson:
CURRENT PLLING DAIE: 2001-06-06
PRIOR PLILNG DAIE: 1998-07-23
PRIOR APPLICATION NUMBER: PCT/US98/15228
PRIOR PLLING DAIE: 1998-07-23
PRIOR PLLING DAIE: 1998-07-23
PRIOR PLLING DAIE: 1998-07-23
PRIOR FILING DAIE: 1997-07-23
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OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
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OTHER INFORMATION: "n" means either a, c, t, or g
                                                                                                                                                                                                                                               NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REGISTRATION NUMBER: 20264126PCT
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 756-4800
TELEPAN: (212) 751-6849
INFORMATION FOR SEQ 1D NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/952,796
                                                                                    08/257,963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
APPLICATION NUMBER: 08/36 FILING DATE: 30-DEC-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/29
                                                                                                                                                                                             FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
                                                                                                                 07 - JUN - 1994
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SOFTWARE: Patentin Ver. 2.1
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LOCATION: 1...224
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                                                                               TELEFAX:
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18 09-497 406-3
18 09-497 406-3
2 Sequence 3, Application US/09797906
2 Sequence 3, Application US/09797906
3 Sequence 3, Application US/09797906
3 Sequence 4, Application 6329188
4 Calebrai INDEMATION 1 ISOLATED HUMAN PROTEASE PROTEINS, ELICE OF INVENTION 1 ISOLATED HUMAN PROTEASE PROTEINS, AND 1 TITLE OF INVENTION 1 USES THEREOF ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND 1 TITLE OF INVENTION 1 USES THEREOF 1 TITLE OF UNENTION 1 USES THEREOF 1 TITLE OF UNENTION 1 USES THEREOF 1 COUNTY OF 1 TITLE OF UNENTION 1 USES THEREOF 1 COUNTY OF 1 TITLE OF UNENTION 1 USES THEREOF 1 COUNTY OF 1 TITLE OF UNENTIAL OF USES THEREOF 1 COUNTY OF 1 TITLE OF USES THEREOF 1 TITLE OF USES THEREOF 1 COUNTY OF 1 TITLE OF USES THEREOF 1 TITLE OF 1 TITLE 
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TITLE OF INVENTION: Sequences and Antibodies Theoreto
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100.0%; Pred. No. le 10;
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/797,906 CURRENT FILING DATE: 201-03-05 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 4.0
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01-OCT-1996
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COMPUTER: 1BM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/WS-DOS
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APPLICANT: Preder, John N.
APPLICANT: Kloumal, Gregory S.
APPLICANT: Raddy, David A.
APPLICANT: Raddy, David A.
APPLICANT: Truchinas, Winston
APPLICANT: Wolff, Roger K.
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: OTHER INFORMATION: n = A.T.C or G
US-09-797-906-3
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NAME: Fitts, Renee A.
REGISJEATION NUMBER: 35.
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Matches 45; Conservative
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FILING DATE: 01-0CT
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Gaps
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100.0%; Pred. No. 9.6e-11;
iive 0; Mismatches 0; Indels
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CURRENT APPLICATION DAIA
APPLICATION NUMBER: US/08/724.394A
FILING DATE: 01-001-1996
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COGATION: 1..246240
HER INFORMATION: /note+ "HLA.H.CONTIG"
US-08-724-3944-26
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  017957-000100
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US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Patent No. 5872237
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APPLICANT: Isuchibashi, Zenta
APPLICANT: Wolff, Roger K.
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COMPUTER: IBM PC compatible
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TELECOMMUNICALION INFORMATION:
TELEPHONE: 415 576-0200
REFERENCE/DACKES NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                      INFORMATION FOR SEQ 1D NO: 20: SEQUENCE CHARACITERISTICS: LENGTH: 246240 base pairs TYPE: nuclear acid
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not relevant
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APPLICANT: Peder, John N.
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Best Local Similarity 100.0
Matches 45; Conservative
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US-09-128-155-17/c
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US-09-741-150-3/c
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                                                                                                                                          Length 54-240;
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APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchhashi, Zenta
APPLICANT: Wolff, Roger K.
TILLE OF INVENTION: Megabase Transcript Map: No. 5872247e1
TITLE OF INVENTION: Sequences and Antibodies Thereto
CORMESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-00S/MS-LOS
SOFTWARE: Patentin Release #1.6. Version #1.40
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San Francisco
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incharion: 1..246240
chiek inscharion: /note: "HLA H.Chviig"
US 08-724-3948-22
                                                                                                                                          Ouery Match
Best Local Similarity 100.0%; Pred. No. 9.6e
Matches 45; Conservative 6; Mismarches
; LOCATION: 1..246240
; OTHER INFORMATION: /hote+ "HLA-H.CONTIG"
US 08-724-3944-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 44
US-08-724-394A-22
IS-08-724-394A-22
Secure 22, Application US/08724394A
Patent No. 5872237
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not relevant
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Matches 45; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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GENERAL INFORMATION:
APPLICANT: GUEGLER, KATL et al
APPLICANT: GUEGLER, KATL et al
TITLE OF INVENTION: USCLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE PREFERICE: CLOOUSG88
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT FILING DATE: 2000-12-21
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APPLICANT: Pan. York
TITLE OF INVENTION: MODES UP TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                    GENERAL INFORMATION:
APPLICANT: Lee, Mu En
APPLICANT: Macmure, Koji
APPLICANT: Hsteh, Chung-Ming
TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REFERENCE: 05443/037001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 18454 CCTTGGCCTCCCAAAGIGCTGGGTTACAGGCATGAGCCACTGC 18411
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100.0%; Pred. No. 3.1e-10;
ative 0; Mismatches 0;
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100.0%; Pred. No. 2.8e-10;
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Best Local Similarity 100.0%; Pred. No. 2.e
Best Local Similarity 100.0%; Mismatches
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/374,454
CURRENT FILING DATE: 1999 UB-13
EARLIER APPLICATION NOMBER: US 60/096,515
EARLIER FILING DAIE: 1998-08-14
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fast.SEQ for Windows Version 4.0
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Patent No. 6117654
Sequence 20, Application US/09374454 Patent No. 6395548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : NAME/KEY: misc_fcature
. LOCATION: (1) ... (112332)
: OTHER INFORMATION: n ~ A,1,C or G
US-09-741-150-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09741150 Patent No. 6436689
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Best Local Similarity 100.0
Matches 44; Conservative
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us-09-846-456-3.oli30.rni

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MOLECULE TYPE: CONA FEATURE:
                                                                                                                                    Query Match
                                                                                                                                                                           Matches
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, HRONSIEIN, BOHEKIS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DN 45158 CCTIGGCCTCCCAAAGTGCTGGGAFTACAGGCAFGAGCACTGC 15115
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APPLICANT: SENOO, Masabaru
APPLICANT: MATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NOMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Pacentin Release #1.0, Version #1.24
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/06/471,570
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
FRICK APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/128.155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091.650
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER: OF SEQ ID NOS: 18
                                                                                                                                                    SCHTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 17
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-INDS
                                                                                                                                                                                                                                                                                                  : LOCATION: (1)...(176373)
: OTHER INFORMATION: n - A.T.C or G
US-09-128-155 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s Sequence 9, Application US/08471570 : Patent No. 5750371 : GENERAL INFORMATION:
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REGISIRATION NUMBER: 29822
REFERENCE/FOCKET NUMBER: 40:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617)523-6440
TELEFX: 200291 STRE UR
INHORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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AITORNEY/AGENT INFORMATION:
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
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                                                                                                                                                                                                                                          OKGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                 1.5%; Score 43; DB 1; Length 2310;
100.0%; Pred. No. 9.2e-10;
12ve 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: DAVID G. CONLIN: DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                     1198 GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCC 1240
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MEDIUM TYPE: Floppy disk
COMPUTER: IMM FOR COMPALIBLE
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NOADA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-10/1995
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: IGARASHI, Koichi
APPLICANT: SENDO, Masaharu
APPLICANT: SENDO, Masaharu
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE AUDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US/08/149,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 07/74 1369
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RECISTRATION NUMBER: 29822
REFERENCE/DCOCKET NUMBER: 40897
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08471570 Patent No. 5750371 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-AUG-1991
ATTORNEY/AGENI :NFORMATION:
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TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
                                                                                                                               43; Conservative
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STRANDEDNESS: double
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Best Local Similarity
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                                                                                                         Hest Local Similarity
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: LOCATION: 25...
US-08-471-570-7
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; NAME/KEY:
; LOCATION:
US-08-471-570-9
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TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
FILE REPERENCE: ISPH-0439
CURRENT APPLICATION NUMBER: US/09/496,694B
CURRENT FILING DATE: 2000-02-02
PRIOR APPLICATION NUMBER: 09/286,407
PRIOR APPLICATION NUMBER: 09/163,162
PRIOR PILING DATE: 1998-04-05
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEO ID NOS: 249
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CURRENT APPLICATION UNDHER: US/09/341,587
CURRENT FILING LAIE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/UE98/00096
EARLIER FILING INTE: 1998-01-09
                                                                                                                                                                                                  Ouery Match 1.5%; Score 43; DB 4; Lo
Best Loral Similarity 100.0%; Pred. No. 8.4e-10;
Matches 43; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 8.4e-10;
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; Patent No. 6335194
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/09341587 baten No. 6346606 GENERAL INFORMATION: APPLICANT: Mollenhauer, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : NAME/KEY: CDS
: LOCATION: (119%5)...(12044)
US-09-496-694B 3
                                                                                                           : NAME/KEY: CDS
: LOCATION: (11955)...(12044)
US-09-630-706-10
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    (2811)...(2921)
                                           (3174)...(3283)
                                                                  NAME/KEY: CDS
LOCATION: (5158)...(5275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Eric E. Swayze
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (28)
NAME/KEY: CDS
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US-09-341-587 7
    LOCATION:
NAME/KEY:
                                                  LOCATION:
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                                                                                                                                                                           APPLICANT: Altieri, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROFEIN THAT INHIHITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MEDICINES
NUMBER OF SEQUENCES: 35
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Patent No. 6277640

CENERAL INFORMATION:
APPLICANT: C. FTAIR Benett
APPLICANT: C. FTAIR BENEELT
APPLICANT: C. FTAIR BENEELT
TITLE OF INVENTION: ANTISENSE MODULATION OF HER'S EXPRESSION FILE REFERENCE: RTS-0053
CURRENT FILING DATE: 2000-08-01
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2417 GGCTGCCAAAGTGCTGGGATTACAGGCATGAGGCACTGGGGC 2375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.6, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,080
FILING DATE: 20-NOV-1997
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1.5%; Score 43: 104:3
Best Loral Shillarity 100.0%; Pred. No. 8/36
Matches 43; Conservative 0: Miscarchas
                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
STREET: 1800 M Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/031,435 FILLING DATE: 20-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                Sequence 35, Application US/08975080; Patent No. 624553; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/FOCKET NUMBER: 044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-467-7000
TELEFAX: 202-467-7176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-08-01
94
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: McLECULE TYPE: DNA (genomic)
US-08-975-080-35
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                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14796 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                                             Washington
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US-09-630-706-10
                                                                                    US-08 975-080-35
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Gaps
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APPLICANT: Chen, H.
APPLICANT: Freiner, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISCRDERS
FILE REFERENCE: 7853-138
                                                                                                                                                             APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND FREATING CHROMOSOME-18P RELATED DISORDERS
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                                                                                                                                                                                                                                                     FILE REFERENCE: 7853.138
CURRENT APPLICATION NUMBER: US/U9/268,992
CURRENT FILING DATE: 1999.03.16
EARLIER APPLICATION NUMBER: 09/236,134
EARLIER FILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER FILING DATE: 1998-10-28
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER FILING DATE: 1998-05-05
EARLIER APPLICATION NUMBER: 60/078,044
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FASTERD for WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/657,474
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/268,992
PRIOR FILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-01-22
PRIOR PPLICATION NUMBER: 60/216,134
PRIOR PILING DATE: 1999-01-22
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/008,312
PRIOR PLING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/008,312
PRIOR RILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
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LCCATION: all n positions
COTHER INFORMATION: n-a, c, q, or t
US-09-268-992-7
                                                                                          Sequence 7, Application US/09268992
Patent No. 6342351
GENERAL INFORMATION:
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US-09-657-474-7/c
: Sequence 7:
Patent. No. 6199762
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Best Local Similarity 100.(
Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 72604
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                                                                         JS-09-268-992-7/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Sequence 18, Application US/09780649
Sequence 18, Application US/09780649
Sequence 18, Application US/09780649
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Myatt
APPLICANT: Jacqueline Myatt
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
TITLE OF INVENTION: ANTISENSE MODULATION OF HOSPHOLIPASE A2, GROUP VI (CA2+-INDEPEND
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0220
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                                                                                                                                                                  Length 25720;
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                                                                                                                                                               Ouery Match 1.5%; Score 43; DB 4; Lk Best Local Similarity 100.0%; Pred. No. 8.1e-10; Matches 43; Conservative 0; Mismatches 0;
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Pred. No. 8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: RTS-0134
CURRENT APPLICATION NUMBER: US/09/783,649
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILLING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.58;
SOFTWARE: Patentin Ver. 2.1 SEC ID NO 7 LENGTH: 28720
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                                                                                          : ORGANISM: Homo sapiens
US-09-341-587-7
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Matches 43; Conserv
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                                                                         TYPE: DNA
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: polymorphic base A or G
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               : polymorphic base C or
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                                                                                    : polymorphic base C or
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NAME/KEY: PITIGE_Bind
LCOATION: 42219.,43237
OTHER INFORMATION: 20-841-149.mis complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 12029. 12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bird
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 19902..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863.45883
OTHER INFORMATION: 20-842.rp complement
NAME/KEY: primer_bind
LOCATION: 76644.76664
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.rp complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 20-853.rp complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 15222. 15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: 20-853-415
NAME/KEY: primer_bind
LOCATION: 929.949
OTHER INFORMATION: 20-828.pu
                                                                                                                                  LOCATION: 42218
OTHER INFORMATION: 20-841-149
                                                                                                                                                                                                                                 OTHER INFORMATION: 20-842-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 20-841.rp
NAME/KEY: primer_bind
LOCATION: 45328..45347
       OTHER INFORMATION: 17-42-319
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250
NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
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LOCATION: 42572..42591
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LOCATION: 1220..1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: primer_bind
                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 77058
                                                                                                                                                                                NAME/KEY: allele
LOCATION: 45442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BIRDIAIN, BETHATG
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Booqueleret, Lydic
APPLICANT: Booqueleret, Lydic
APPLICANT: Booqueleret, Lydic
APPLICANT: Booqueleret, Lydic
APPLICANT: Salter-cid, Ludsa
APPLICANT: Salter-cid, Ludsa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBIT:NG NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89.052.CIP
CURRENT APPLICATION NUMBER: US 09/599,362
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 2000-06-21
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 60/113,685
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
PRIOR FILING DATE: 1998-12-22
                                                                                                                                                            Gaps
                                                                                                                                                            0
                                                                                                           Length 72604;
                                                                                                                                                         0: Indels
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LOCATION: 12347
                                                                                                                                                                                                                                    Db 63856 GCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCC 63814
                                                                                                                                                                                                       Oy 1199 GCCTCCCAAAGTGCTGGGATTACAGGCATGAGGCGATTGGGGCC 1241
                                                                                                      1.5%; Score 43; DB 4; Le
100.6%; Pred. No. 7.8e-10;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 14271...15968
OTHER INFORMATION: exon 4
NAME/KEY: misc.feature
LOCATION: 15969...17969
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory regio::
DOCATION: all n positions (OTHER INFORMATION: n-a, c, g, or t. US-09-657 474-7
                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09750580 Patent No. 6455280 GENERAL INFORMATION: APPLICANT: Yen, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yen, Frances
Denison, Blake
Bour, Barbara
Bihain, Bernard
                                                                                                                                                       43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 12947..12958
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LOCATION: 13470..13526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13641..13752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: INCMBER OF SEQ ID NOS: SOFTWARE: Patent.pm
                                                                                                                                Best Local Similarity
Matches 43: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
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LENGTH: 81001
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US: 09-750-580-1
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                                                                                                           Query Match
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Gaps
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                                                                                                                                                                                                                                                                   Length 98844:
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APPLICANT: Donna I: Ward
APPLICANT: Andrew T: Ward
APPLICANT: Andrew T: Wart
ITILE OF INVENTION: ANIISENSE MODULATION OF RECOL2 EXPRESSION
FILE REFERENCE: RTS-0207
CURRENT APPLICATION NUMBER: US/09/798,096
CURRENT FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5%; Score 43; DB 4; Length 93500
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                Db 55998 GCCACCTTGGCTCTCAAAGTGCTGGGATTACAGGCATGAGC 55956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY 1198 GCCTCCCAAAGIGTGGGGTTACAGGCATGAGCACTGCGCC 1240
                                                                                                                                                                                                                                                                                                                                                         1189 GCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGC 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08812204
Patent No. 5965790
GENERAL INFORMATION:
GENERAL ACTION:
GENERAL ACTION:
APPLICANT: Action, Susan L.
TITLE OF INVENTION: SR-BI REGULATORY SEQUENCES AND
TITLE OF INVENTION: THERAPFUTIC METHODS OF USE
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,204
FILING DATE: 06-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 7.7e-10; Mismatches 0;
                                                                                                                                                                                                                                                                   1.5%; Score 43; DB 4; L
100.0%; Pred. No. 7.7e-10;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: FOLEY, HOAG & ELLOT LLP STREET; One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-798-096-10/c
; Sequence 10, Application US/09798096
; Patent No. 6399478
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100.0%; Pre
0;
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MEDIUM TYPE: Floppy disk
                     LOCATION: 65471
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 87130
                                                                                                    OTHER INFORMATION: UNKNOWN NAME/KEY: UNSUFE LOCATION: 89049
                                                                                                                                                                          CTHER INFORMATION: UNKNOWN CTHER INFORMATION:
US-09-791-211-10
                                                                                                                                                                                                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100. Matches 43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 43; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: One PC
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Donna T. Ward
APPLICANT: Andrew T. Watt
ITTLE OF INVENTION: ANTISENSE MUDGLATION -F WEN EXPESS: N
FILE REFERENCE: RTS-0205
CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
LENGTH: 98844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 59318 GCCTCCCAAAGTGCTGGGATTACAGCCATGAGCCACTGGGGC 59360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1198 GGCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCC 1240
                                                                               LOCATION: 45443.745461
CTHEK INFORMATION: 20-842-115.mis complement.
NAME/KEY: Primer_bind
LOCATION: 77039.77057
CTHEK INFORMATION: 20-853-415.mis
NAME/KEY: Primer_bind
LOCATION: 77059.777077
                                                                                                                                                                                                                                       OTHER INFORMATION: 20-853-415.mis complement NAME/KEY: misc_binding OCAME/KEY: misc_binding OCATION: 1277...1251 OCHER INFORMATION: 20-828-311.prob**
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_binding
LOCATION: 45430..45454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: 20-853-415, probe US-09-756-580-1
                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_binding
LGCATION: 12335, 12359
OTHER INFORMATION: 17-42-319, probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 48
US-69 791-211-10/C
: Sequence 10. Application US/09791211
: Parent No. 6448080
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 17-41-250.probe
              GGATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_blod
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Hest Local Similarity 100.0
Matches 43; Conservative
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LOCATION: 42206..42230
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LOCATION: 15229. 15253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: primer_bind
GCATION: 45423..45441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: 64.383
UTHER INFORMATION: UN
NAME/KEY: unsure
LOCATION: 65468
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OTHER INFORMATION:
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LOCATION: 65469
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LOCATION: 65470
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CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth 35,430

REFERENCE/DOCKET NUMBER: 35,430

REFERENCE/DOCKET NUMBER: MIA-014.01

TELECHONE: 617-832-1000

INFORMATION FOR EQUIDON: 1:
FELEMAN: 617-832-1000

INFORMATION FOR EQUIDON: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: DNA (genomic)
US-08-812-204-1

QUETY MATCH
HOST CONSERVATIVE 0; MISMATCHES 0; Endeth 10:3;
Hest Local Similarity 100.0%; Pred. No. 2.5e-09;
MAtches 42; Conservative 0; Mismatches 0; Endels 0; Caps
UV 1040 GCCTCCCGGGTTCAAGCGATTCTCCTGCTCCAGCCTCTGAC 10:81

DD 447 GCCTCCCGGGTTCAAGCGATTCTCTGACTCAGCTCTGAC 486
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Search completed: May 10, 2003, 04:39:45 Job time : 4287.72 secs

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Fun on: May 10, 2603, 01:55:23 ; Search time 1947 Seconds	:	Score Match	Length	E :		Descr	Description
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Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.
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Lamir M. Waderbi, Oram, J.F. and Garvin, M.
Alp biding cassette transporter protein abol polypeptides
Paten: We nove971-A 1 28-DBC-2000;
Homo Sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelecsioni;
Mammalia; Eitheria; Primates; Catarrhini; Hominidae; Homo.
Lebass 1 to 10442)
Lawn, R.M., Wade, D. and Garvin, M.
Regulation with binding cassette transporter protein abol
Patent: W: 0078972.A 1 28-080.
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/db_xref "taxon:9606"
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104-2 bp mENA linear PRI 09-AL FORD Sapiers ATP-binding cassette transporter i (AFAI) mENA, complete cds.
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/protein_id-"AAR98175.1"
/db_xreff-"GI:9755159"
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Porter,J.G., Seilhamer,J.J., Vanahan,A.M. and (10)
Direct Submission
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Schwartz,K., Lawn,R.M. and Wade,D.P.
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/db_xret:"taxon:9606"
/chromosome."9"
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NRFGROTT I VVRIAGSNPDI.KPVQDFFGLAFPGSVLKRHNM..QYQILSSILSSIARI
FSII.SGSKKREHIEDYSVSQTTLDQVPVNFAKDGSDDDHLKDI.S..HKNG.IVVJNAVLT
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Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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Regulation with binding cassette transporter protein abol
Patent: Wo 0078972-A 7 28-DEC-2000;
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99.2%; Pred. No. 4.3e-32;
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/dt xrei-"taxon:9606"
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Extracted Metazoa, Chordata: Craniata; Vertebiara Extelessioni;
Mammalia: Extheria: Primates: Catarrhini: Bozoriciou: Homo.
1 (bases 1 to 10474)
I (bases 1 to 7040, D. Oramu, F. and Garvin, M.
Alami, R.M. Made, D. Oramu, F. and Garvin, M.
Alphinding Gassette transporter professionials: projectides
Patent: WO 0078971-A 7 28-ber-2000;
CV PHERAPEUTICS, INC. (US)
                         Homo sapiens
Enkaryota, Metazoa, Chordata, Graniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominide, Homo.
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                                                              l (bases 1 to 10474)
Lawn,R.M., Wade,D. and Garvie,M.
Requiation with binding cassette transporter protein abel
Patent: WO 0078972-A 9 28-DEC-2000;
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/db_xref="taxon:9606"
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2304 c 2415 q 2844
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99.2%; Pred. No. 4
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Matches 127, Conservative
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PRI 17-JUL-2000
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Suntamentine Polo,S., Peterson,K., Knapper,C., Qiu,Y., Ereeman,L.,
Cheng,J.F., Osorio,J., Remaley,A., Yang,X.P., Haudenschild,C.,
Prades,C., Chanini,G., Blackmon,E., Francois,T., Duverger,N.,
Rubin,E.M., Rosier,M., Denefle,P., Fredrickson,D.S. and Brewer,H.B.
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    PAT 22-JAN-2001
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 10474)
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Mammalia, Estheria, Primates, Catarrhini, Hominidae, Homo.
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2 (bases 1 to 149034)
Santamarina-Fojo.S., Peterson.K.M., Knapper.C.L., Freeman.L.A.,
Remaley.A.T., Yang.X.-P., Haudenschild.C.C., Blackmon.E.E.,
Francois, F.L. and Brewer, H.B. Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-JUN-2000) Molecular Disease Branch, National Institutes of Heath, National Heart, Lung and Blood Institute, Bethesda, MD 20892, USA
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Atp binding cassette transporter protein abol polypeptides
Patent: WO 0078971-A 9 28-DEC-2000;
CV THERAPEUTICS, INC. (US)
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Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7987-7992 (2000)
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Pred. No. 4.3e-32;
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KLEFIATEVWLI INKSMEKHWEI PFOIT PERSIEL PHHVKK KIRMUIONVERT
NKI KOGYMDEOFRADFFEDMRYVMGGFAYLODVYEQAIIRVLIGTEKKTGVYMQOMPY
                                                                                                               PCYVDDIFLRYMSRSMPLFWTLAWIYSVAVIIKGIVYEKEARLKETMRIMGLDNSILW
FSWFISSLIPLLVSAGLLVVILKLGNLLPYSDPSVVFVFLSVFAVVIILGGELISTLF
SRANLAAAGGGIIYFTLYLPYVLCVAWQDYVGFTLKIFAXLLSPVAFGFGGEFFALFE
NI.SLPKSTVI)KMLRADV I LHKVFLQGYQLHLTSLCNGSKSEEMIQLGDQFVSELCGLP
              REKIJAAAERVIJRSNMDIIJKPILRTLNSTSPFPSKELAEATKTLLHSLGTLAQELFSMR
                                           GGNGTEEDAETFYDNSTTPYCNDLMKNLESSPLSRIIWKALKP:.LVGK11.YTPDTPAT
                             SWSDMRQEVMFLINVNSSSSTQIYQAVSRIVCGHPEGGGLKIKSLNWYFDNNYKALF
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50547, .50614
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Biochem. J. 350 Pt. 3, 865-872 (2000)
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Ueda,K. Kioka,N. and Tanaka,A.
Ueda,K. Kioka,N. and Tanaka,A.
Direct Submission
Submitted (0.2 FEB-2000) Kazumitsu Ueda, Kyoto University
School of Agriculture, Division of Applied Life Sciences;
Kitabilizakawa, Sakyorku, Kyoto, kyoto 66-8502, Japan
(E-mailisaedarkkalaskyoto-u.ac.jp, Tel:81-75-753-6105,
Fax:81-75-753-6104)
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/db_xret="G1:9711459"
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                         /map="9q31"
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/gene="ABCA1"
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M. Biochem. Brophys. Res. Commun. 271 (2003) In press
E. Chases I to 200)
Pulinger C.R., Hakamata H., Dachateau, I.N., Eng., S., Pulinger C.R., Hakamata H., Dachateau, P.N., Eng., S., Souriert Submission
M. Submitted (23-JUN-2000) Variationascular Research Institute.
University of California, San Francisco, 50% Pariasses Avence, San Francisco, CA 94143-0130, USA
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Mammalia, Eutheria, Primates, Cataribin: Bedinione, Homo.
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/db_xref="taxon:9606"
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68499, .68731
/rpt_family="Alu"
69481, .69760
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61246, .61489
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67123, .67342
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72244, .72501
                                                                           /rpt_tamily-"Alu"
55297. .55344
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64082, .64306
                   /rpt_family="Alu"
55029, .55226
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62812. .63077
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Denelle,P., Rosier-Montas,M.F., Arnouid Requisity i., Praces.C.,
Naudin,L., Lemoine,C., Duverger,N., Jaye,M., Scart.ss [il.s.B.,
Kemaley,A., Brewer,H.B. and Dean,M.
Nucleics acids of the human atc] gene and their titrapentity and
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Denefle,P., Rosier-Montus,M.F., Arnorid Requirection Prades.C.
Naudin,L., Lemoine,C., Duverger,N., Jayo.M., Scattoss,C.B.,
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/note-"Oligonucleotide Primer"
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tive 0; Mismatches
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Patent: EP 1096012-A 3 02-MAY 2001,
Sequence 3 from Patent W00130848.
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Mammalia: Eutheria; Primates: Catarrhin; Hominidae, Homo.
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Porsch degruerienez,M.K.
Direct Submission
Submitted (07-3NN-2000) Forsch-Oezcueruemez M.K., Institute for Clinical Chemistry, University of Regensburg,
Franz-Josef-Strauss-Allee II, 93042 Regensburg, GERMANY
                                                                                                              1 (bases 1 to 480)
Forschinezeueriemez.M., Langmann,T. and Schmitz,G.
Cloning and Characterization of the human ATP-binding Cassette
Transporter-1 (ABC-1) Promoter
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/protein_id-"CAC21428.1"
/db_xref-"G1:1416345.
/translation-"MACWPOLRILLWKNLTFRRRQT"
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/db_xref-"taxon:9606"
/chromosome="9"
/map-"9931"
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189. 346
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Pinus radiata PAL Plant PAL enzyme D

Pine phenylalanine

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	AAD37269 standard; DNA; 159 BP.
	AAD37269;
	21-AUG-2002 (Tirst entry)
	Human ABCl gese exon 18 DNA.
	Human: ATP-binding cassette 1; ABCl gene regulation; atherosclerosis;
	cholesterol metabolism; hypercholesterolaemia; antisense therapy; exon 18; qene; ds.
	Homo sapieus.
	Key localithers CDS 94159
	WO200183746 A2.
	08 - NOV - 2001.
	02-MAY-2001; 2001W0-EP05488.
	02-MAY-2000; 2050US-201280P.
	(AVET ) AVENTIS PHARMA SA.

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metabolism, including diseases such as atherosclerosis. Polynucleotides of the invention are used to screen candidate molecules or substances that are capable of modulating the transcription of the ABCI gene. They are used in antiscuse therapy, Compositions comprising sequences of the invention are used to treat hypercholesterolaemia and atherosclerosis.
                                                                             The invention relates a nucleic acid which is capable of regulating the transcription of human ATP-binding cassette 1 (ABC1) gene, which is a casual gene for pathologies linked to a dysfunctioning of cholesterol
(ABC1) and screening for candidate modulatory compounds or substances
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poblipoprotein-mediated mobilisation; cholesterol: Tangier disease;
chromosome $422-9441; heart, disease; hypercholesterolemia;
atherosclerosis; cholesterol transport; ss.
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/product= "ABC1 polypeptide"
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               tus M. Prades C. Lomoine C. Naudin L. Dem
Duverger N. Remaley A. Santamarina-Fojo S.
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Brewet B. Duverger N. Remaley A. Santamarina-Fojo S.
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 159 BP; 32 A; 47 C; 48 G; 32 T; 0 other;
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                                                                                                                                                                            Claim 5: Page 132; 152pp; English.
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Matches 159; Conservative
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               Posier-Montus M,
                                                                              P-PSDB; AAE22999
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                             Brewer
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useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolems and
                                                                            The present sequence encodes a human adenosine triphosphare (AIP) binding cassette protein (ABC) I polypeptide. ABCI resids in cell membranes and utilises ATP hydrolysis to transport a wise variety of substrates across the plasma membrane. ABCI is a protein mediated mobilisation of intracellular obclein in the apolipoprotein-mediated mobilisation of intracellular obclein in strones. ABCI is defective in Tanajer disease, a quelic diseascier claracterised by abnormal BDE-cholestero inetabolism. The ABCI quells localised to chromosome 9422-9431. The ABCI quees and proteins are
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polipoprotein-mediated mobilisation; cholesterol: facilio disease;
enfomosome 9422-9431, haart disease; hypercholesterolenia;
atherosclerosis; cholesterol transport: ss.
                                                                                                                                                                                                                                                                                                                    48.4%; Score 77; Db 22; Lanath P412; 99.2%; Pred. No. 6.50-29;
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                                                                                                                                                                                                                                                                                                                                               X 137011
                                                                                                                                                                                                                                                                  other disorders associated with hypercholesterolemia.
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                                                     bisclosure: Page 122-128; 215pp; English.
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Matches 127, Conservative
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(49 GACAAACA 356
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14 SEP - 1999;
19 NOV - 1999;
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disease and other disorders associated with hypercholesterolemia and atherosclerosis. The genes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated
                                                                                                                                                                      Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide. ABCI resides in cell membranes and ultilises AFP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in Tangier disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABCI quie is localised to chromosome 9422-941. The ABCI genes and proteins are useful for developing pharmaceutical agents for the treatment of heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with cholestero, transport. The genes and proteins are also useful for are also useful as diagnostic indicators of cardiovascular disease and other diseases associated with hypercholesterolemia.
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Garvin M;
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Pred. No. 6 Ser29;
Fridam of the Ser2
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99US-0153872.
99US-0166573.
                                                                                                                                   16-JUN-2000; 2000WO-US16765.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (CVIH ) CV THERAPEUTICS INC
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Matches 127; Conservative
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14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                       19-NOV-1999;
                                          28-DEC-2000
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The present sequence encodes a human adenosine triphosphate (AIP)

binding cassette protein (ABC) I polypeptide, and is isolated from
a Tangler disease patient. ABCI resides in cell membhanes and utilises
a Tangler disease patient. ABCI resides in cell membhanes and utilises
blasma membrane. ABCI is a pivotal protein in the apolipoprotein-mediated
mobilisation of intracellular cholesterol stores. ABCI is detective in
Tangler disease, a genetic disorder characterised by abnormal
HDL-cholesterol metabolism. The ABCI gene is localised to chromosome
of 942-9431. The ABCI genes and proteins are useful for developing
pharmaccutical agents for the treatment of heart disease and other
disorders associated with hypercholesterolemia and atheroscierosis. The
genes are useful for developing screening assays to screen for compounds
that regulate the expression of genes associated with cholesterol
transport. The arenes and proteins are also useful for are also useful
as disquestic inhibitators of cardiovascular disease and other disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
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0; Mismatches 1; Indels
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99.2%; Pred. No. 6.5e-29;
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Location/Qualifiers
323.,7108
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Matches 127; Conservative
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381 GACAAACA 348
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AAF24708 standard: DNA; 10474 BP
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Bost Local Stanlarity 99.2
Matches 127. Couscivalize
381 CACAAACA 388
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                   Nucleotide sequence of ABC1 polypeptide from langier disease patient
                                                     Human: ademosine triphosphate binding cassette profeir. 1. ABC1; apoli poprotein mediated mobilisation; cholesterol; Targico disease: chromosome 5q22-9q31; heart disease; hypercholesterolemia; atteroscierosis; cholesterol transport; ss.
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                                                                                                                                                                                                                                             /product= "defective ABC1 polypeptide"
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99.2%; Pred, No. 6.5e-29;
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99US-0166573.
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19 NOV 1999;
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The present sequence encodes a human adenosine triphosphate (ATP) binding cassette protein (ABC) I polypeptide, and is isolated from a langiar disease pattent. ABCI resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the piasma membrane. ABCI is a pivoral protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABCI is defective in
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                                                                                                                                          Nucleotide sequence of ABC1 polypoptide from Tangier disease patient.
                                                                                                                                                                                                                                              apolipoprotein mediated mobilisation; cholesterol; Tandici disease; chromosome 9422-9431; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
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Pred. No. 6.56-29; |
Pred. These | 1; | Indels
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990S-0166573.
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19 - NOV - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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Naudie L:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which encodes amino acids 1-60 of the human AMM protein. The nuclear acid sequence, primers and probes derived from the AMM sequence, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transport of cholesterol. The nucleic acids and polyper des are also
AGARGAA 15:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human AbCl protein, amino ands i to 60"
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                                                                            1.1 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating and preventing cardiovascilar and he contained pathologies, and other diseases e.g. identer disease, e.c.infinite
                                                                                                                                                                                                                                                                                                                                              Human: ABC1 qene; atherosclerosis; reverse transport; Pholesterol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence represents the partial coding sequence of Junea ABCL
                                                                                                                                                                                                                                                                                                                                                          cardiovascular; neurological; Tangler disease; LCAT delbiency;
lecithin cholesterol acetyltransferase; malaria; diaketus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human Abdi bucleic acids and polypopions for treature
                                                             ACA TOGINATORAGE CARGAGET GET GET GET GET GET GET FOART FOART TO
                                                                           3 M. Arnould-Requique 1 Francisco Jaye M. Scartoss 68. Repale.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualitiers
                                                                                                                                                                                                                                                                                                                Partial human ABC1 cDNA sequence.
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                                                                                                                                                                                                                                                                                   (tirst entry)
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                                                                                                                      152 GACARACA 159
                                                                                                                                     SEL GAGAAGA 388
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                                                                                                                                                                                              RESULT 3
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Sequences ABBIU981-ABB12330 represent 1350 novel human polypeptides, and sequences ABAG8225-ABAU9574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of identifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which polypeptides to the invention and nethods of identifying compounds which prolypeptides of the invention have bomological activities, and honce potential therapeutic applications. The polypeptides of the invention may have various activities including eytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; have various activities; stem cell growth factor activity; mmunomodulatory activity activity activity activity activities; hambon-related activities; chemostatic or chemostatic activities; hambon-related activities; controlled in our accesses, concert cell proliferation or metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                      Human, cytokine: cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bone disorder; osteoporosis; vascular growth disorder;
tissue reqeneration; wound healing; infection; immune disorder;
cell culture; drug screening; wene therapy; antiinflammatory;
antiasthmatic; dutianthritic; hemostatic; antianteriosolerotic;
cytostatic; osteopethic; vasotropic; caidiant; virucide; antibacterial;
antitungal; vulcerary; antialcer; ss.
                                                                                     HELLIH HELLIH HELLIH HELLEH HELLEH HELLEH HELLEH HELLE BETTAGARANAGA CASO 191 TGITGGGCH GAGG GAGGGGGGGGGAAGAACCT CACT TACAGAACAAGAACAA 250
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins and DNA encoding sequences useful for proventing, treating or ameticaling a medica, condition in a mammalian subject
                    6
                      Indels
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Pred. No. 2.1e-20;
                      Mismatches
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                                                                                                                                                                                                                   ABA09200 standard; conA; 7086 BP
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100.08;
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                    Conservative
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Best Local Similarity
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                      Matches
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Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or decilorating medical conditions, e.g., by protein or gene therapy. Such confidence include canders, haematopoictic disorders (e.g., myeloud or lynginsid cold disorders), chronic inflammatory conditions (e.g., assume or artiritis), profiferative retinopathy, atheroscierosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and absorbal vascular growth, Polypeptides involved with tissue reaccention and
                                                                                                                                                                                                                                                                                   that can be used to addment or replace cells damage by . Incss. autoimmune disease or accidental damage. The polypoptics and marketimes may also be used in the diagnosis of the akeye conditions, and in drug screening techniques. The present segione represents a cisM exemina a
                                                                                                                                                  repair (or nucleic adds encoding them) may be used to promote wound becaling (e.g., of burns, incisions and ulcets), while these with immunonabilatory activities may be used in the treatest of viral bacteria; and fungal infections in addition to immune ensureders. Prypeptiates with growth factor activity may be used in each onlines to promote cell growth. For example, such pulypeptiates must be used for municipalist stem cells in culture to give rise to represent belief
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haman: eytokine: cell proliferation: cell differential () qene therapy:
Vacrine: peptide therapy: stem cell aroxim factor: has be acciesis;
tissue growth factor; immunomodulatory; cancer; leikachia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        32.7%; Score 60; LH 22; Length 7 80;
Hest Local Similarity 100.0%; Pred. No. 2.16-20;
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                                                                                                                                                                                                                                                                                                                                                                 novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK% 2667 standard; cDNA; 7086 BF
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2000US - 0620325.
2000US - 0654936.
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2000US-0560875.
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2000US-0693325.
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19-JUL-2000;
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27-APR-2000;
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20.OGT-2000;
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                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity eleting to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth tactor activity, immunomodulatory activities, activity, issue growth lactor activity, immunomodulatory activity and activity inclinibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: ATP brinding cassette transporter 1: ABC1; coronary legat disease; dermatological; atherosclerosis; cardiovascular; inflammatory disease; psoriasis; high diseader; antibacterial; septic shock; get; therapy; immuosuppressive; lupus crythematosus; rheumatoid arthritis; ds.
                                                                                                                                                                                                                                               treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                   (AAM80020) are emitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Records for SEQ 10 NO 2110 (AAK52581), 2111 (AAK52582) and 4666
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Nacheic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                       Sequence 7086 BP: 1773 A; 1739 C; 1859 G; 1715 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human ATP binding cassette transporter 1 (ABC1) gene.
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Fred. No. 2.1.
Matches 50; Conservative 0; Mismatches
                                                  Claim 1; Page 4558-4560; 6221pp; English.
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P-PSDB; AAE13022.
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                                                                                                                                                                                                                                                                 inflammation.
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Example 1: Fig 1: 48pp: Endlish

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Homo sapiens
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20-OCT-2000;
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      The invention relates to four common polymorphisms in the gene encoding APP-binding cassette transporter-1 (ABC1). ABC1 is associated with decreased ApoA1 mediated efflux of cholesterol. The polymorphisms in ABC1 directly affects cellular liptod homeostasis, which is a key fartor in the atherogenetic processes. The ABC1 polymorphisms are useful for diagnosing and treating lipid disorders, cardiovascular 1. Seases (coronary heart disease, atherosclerosis) and intlammatory diseases (psortasis, lupus erythematosclerosis), diagnosing and transporter for interleukin-libeta (1. Deta) identities this gene as a candidate for interleukin-libeta (1. Deta) identities this gene as
                                                                                                                                                                                          100 IGTTGGCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAJAAJAGAAAAAA 159
                                                                                                                                                                                                       0: Gaps
                                                                                                         arthritis and septic shock. The present sequence is human ABCI gene.
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/note= "alternative open reading frame of AAI70814"
                                                                                                                                                                                                                                                                                                                                                             cholestero); cardiovascular disease; inflammatory disease;
antificflammatory; antilipaemic; antipsoriatic; demuticleafed
Tangier disease; coronary heart disease; diaquosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                   AlP binding cassette transporter 1; ABC1; human; lipid disorder;
                                                                                                                                                    Length 27600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New adenosine triphosphate binding cassette transporter reae
                                                                                                                                Sequence 7260 BP; 1834 A; 1765 C; 1905 G; 1756 T; a other;
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                              Human ATP binding cassette transporter 1 (ABC1) cDNA.
                                                                                                                                                    DB 22; 15
. 2.1е 26;
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                                                                                                                                                                        0; Mismatches
                                                                                                                                                    37.7%; Score 60; 100.0%; Pred. No.
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321..7106
                                                                                                                                                                                                                                                                  AA170315 standard; cDNA; 7260 BP
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replace(3836,C)
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                                                                                                                                                            Best Local Similarity 100.0
Matches 60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           polymorphism; ss.
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Human; cytokine: cell proliferation; cell differentiation; gene therapy; vaccine; peptidet hierapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; sa.
                                                                                                             100 TGTTGGCCTCAGGTGAGGTTGGTGGTGGAAGAACGTGACTTTCAGAAGAGAGAAAACA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      control subjects. The use of the provided ABCI polymorphisms for the diagnosis and treatment of lipid disorders, cardiovascular diseases, and inflammatory diseases (e.g. psoriasis, lupus erythematodes) is cialimed. Modulation of ABCI transcripts or proteins by antisense or ribozyme technology or RNA decoys is also
polymorphisms, useful for diagnosing and treating lipid disorders, cardiovascular diseases and inflammatory diseases
                                                                                                   present sequence is that of cDNA encoding the human adenosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7260 HP; 1834 A; 1765 C; 1905 G; 1756 T; 0 other;
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37.7%; Score 60; DB 22; Lv
100 0%; Pred. No. 2.1e-20;
                                                           Disclosure: Page 26-28; 41pp; English,
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100.0%; Pre
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2000US - 0560875,
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20000S-0620325,
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20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
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Wilson AR, Pimstone SN;

dayden MR,

WPI; 2000-587528/55. P-PSDB; AAB38107

(VYBR-) UNIV BRITISH COLUMBIA.

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The invention relates to polynucieotides (AAK51495 AAK6518) and the encoded polypeptides (AAM78323-AAM80302) that exhibit delivity dealing to eytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or poptide therapy. The polypeptides have various cytokine, the delivities, e.g. stem cell growth factor activity, harmatopolesis is anolating activity tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosts and/or treatment of cancer, leukaemia, nervous system disorders atthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ABC1 cholesterol transporter; chromosome 5453.

ATP-binding cassette; HDL deficiency disorder; hosh duscry Experterion; Tanarier disease; TD; familial HDL deficiency; FNA: polyerphism: cardiovascular disease; coronary aftery disease; chromary erespectives; restenosis; cerebrovascular disease; peripheral vascular disease; peripheral vascular disease; however, fresciency additional alientation of the first disease; find additional a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytoxine-like intuities useful in diagnosis and gene therapy ^{\circ}
                                                                                                                                                                                 Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R;
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30-NUV-2000; 2000US-0728422.
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                                                                                                                                                                                                                                                                                                                                                                       WPI: 2001-476283/51.
                                                                                               (HYSE-) HYSEQ INC.
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17-JUN-1999;
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The invention relates to the human ABC1 cholesterol transporter protein (1938082) and to nucleic acid sequences (C69120) which encode it. ABC1 is a member of the ATP-hinding cassette (ABC transporter) superiamily of proteins, and plays a crucial role in cholesterol transport, particularly components, and plays a crucial role in cholesterol transports, being involved in cholesterol efflux from the cell. The gene encoding ABC1 is coated on chromosome 9q31, and mutations in this gene are associated with two genetic HDL (high density lipoprotein) deficiency disorders. Tangier disease (TD) and familial HDL deficiency (FHA). These diseases are distinguishable in that TD is an autosomal recessive diseases are distinguishable in that TD is an autosomal recessive disease. CC FHA is inherited as an autosomal dominant trait. Low levels of HDL (good correlate with a high risk of cardiovascular disease, particularly octonary artery disease, but also cardiovascular disease. Conversely, a high level of HDL has protective effects against disease, coronary restences; and peripheral vascular disease. CC cardiovascular disease. CC cardiovascular disease. CC cardiovascular disease comprising the administration of an expression vector encoding ABC1 or an active fragment thereof. The invention also compusases compounds which mine ABC1 expression and methods of screening for such compounds. CC stimulate ABC1 expression and methods of screening for such compounds. In the mine disease due to polymorphisms in the increased risk for cardiovascular disease. CC repression and nucleotides can be used to treat or prevent cardiovascular disease. CC or performer a patient was in the compense of the proper and active fragment disease. The reference or performer disease. CC or prevent corporary restances or propered corporary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents cDNA encoding a mutant human AbCl cholesterol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transporter associated with an altered cholesterol level and therefore altered risk of cardiovascular disease.
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                                                                                                                                                                                                                                                             New ABC1 polypeptide is useful for treating diseases associated with ABC1 biological activity, e.g. Alzheimer's disease, Huntington's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The present sequence is not shown in the specification, but is derived from the native human ABCI cDNA shown on pages 157-169.
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Best Local Similarity 100.0%; Pred. No. 2.2
Best Local Similarity 100.0%; Mismatches
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A0709464 HS\_S459\_A A0953274 A0953274 B0259614 rad02b03. A4495487 fac9h12.r A1497295 fbc19d4.y A0997283 A0997283 B1160520 602664591

AWII6004 f:06all.x BF898523 CM:-MT018 BH402163 AG-ND-102

AA098714 T4026 MVA

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AL698654 EST 21-MAR-2002 MRNA linear EST 21-MAR-2002 DKF27686812109_r; 685 (synonym: hlcc3) Homo sapiens cDNA clone DKF27686N12109 5', mkNA sequence.
AL696654
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Ducsterboett, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo Sapiens
Eukarycta, Metazon: Chordata: Craniata: Vertebrata; Euteleostomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Am Klopterspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ): Email s.wiemann@dkfz-heideiberg.dc;
sequenced by Qiaqen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone (DKF2p686N12109) is available at the R2PD in Berlin.
Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                           AL I GNMENTS
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BO751693
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AH396354
AO779444
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AY067297
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BI996668
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BQ751274
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Unpublished (1999)
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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        GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.
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HRI buman cDNA project; 5. 6. 4' end one pass separation: Belix
Research Institute; cDNA library construction: by ethert of
Vitology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                              /close_lib=fectoring skeletai mescie*
/tissue_type="human skeletai mescie*
/dev_stage="adult"
/lab_host="HH0B"
/note="vector: pTriplEx2: Site_li St::A: S:te_2: Sfilis;
rbNa=collection*
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Yamamoto,J., Wakamatsu,A., Nakamini,Y., Naselli, S
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Teis 81-438-52-3975
Fax: 81-438-52-3986
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/note="Vector: pME185FL3"
199 c 199 g 120
                                                        /organism-"Homo sapiens*
/db_xref="taxon:9606"
/clone-"DKF2p686N12109"
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HRI human cDNA project
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Genemics Laboratory
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ilarity 99.28;
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Single pass sequencing, Bases called and alt_trimmed with phred v0.980904.c. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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Pabrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
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/dlone_lib-"MARC_lPIG"
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/lab_host "bullOB"
/acto="Voctor: pCMV_SPORT6; Site_1: Not1; Site_2: Sal1;
Library made_from pooled_tissue_from_day_ll_i3, 15, 20,
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Enküryolu: Metavoa: Chordala: Craniala: Vertebrata: Euteleostomi:
Masmulia: E.C.ecia, Primates: Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
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109 CAGCTGAGGTTGCTGCTGTGGAAGAACCTCACTTTCAGAAGAAGAAAACA 159
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                    Indels
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PO Rox 166. Clay Center, NE 68933-0166, USA
Tel: 402 742 4366
Eax: 402 762 4360
Email: Smithfemail.marc.usda.gov
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100.0%; Pred. No. 4.9e-09;
UVe 0; Mismatches 0;
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Seq primer: ATTTAGCTGACACTAIAG.
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Mammalia; Eutheria: Frimates: Catarthini; Hominidae; Homo.
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Rua Prof. Antonio Prodente 109, 4 andar, 01509-010, Sao Paulo SP,
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20202664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chare_lib-"Marmailted Chicken
Pitulitary/Hypothalamus/Pineal Library"
Email: cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                            /strain-"Commercial broiler chicken"
/db_xref-"taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host-"E. Coli EMDH108"
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Fax: -55-11-2707001
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Small A mini-library was made by cloning products delived trom ORESTES PCR (U.S. Letters Patent application No. 195 776 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under 10% stringency conditions."

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45 Owen Anne Avenue North, Seattle, KA belov. 26
101. (206) 616-368
Fax: (206) 616-3887
Fmail: jwallace@u.washington.edu
Fnotes may be purchased from Research Genetics ( Bhofresagn.edu).
HAC end Web Server: http://www.htsc.washington.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enteleostomi;
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Eukaryota; Metazoa: Chordata; Craniata; Vertetisis - Futeleostomi;
Mamaila; Eutheria; Primates; Catarrhini; Healinses; Homo.
1 (Gases 1 to 454)
Mahairas, G.G., Wallace, J.C., Smith.K., Swartzell s., Holzman.L.,
Mahairas, G.G., Wallace, J.C., Smith.K., Swartzell s., Holzman.L.,
Mahairas, G.S., Shaker, R., Furionq.J., Young.D., Zhan.Z., Adams.M.D., a.
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/note="Vector: pBACe3.6; KPUIll Human Male 5AC Library"
1 82 c 90 g 135 t 2 others
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Bigh Throughput Sequencing Center
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Pred, No. 51;
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Matches 19; Conservative
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                                                                                                                                                                           Eukaryola Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi; Actinopteryali: Nechterygii; Teleostei: Ostariophysi: Cypriniformes; Cyprindae: Danzo.
1 (bases 1 to 470)
Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and Liew
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/db_xer="taxon:7955"
/db_xer="taxon:7955"
/clouse_lib="Zebratish Embryonic Heart cDNA Library"
/dev_stage="embryonic day 3 post-fertilization"
/dev_stage="embryonic day 3 post-fertilization"
/dev_stage="embryonic Heart Vector lambda ZAP Express: Site_l:
Ecoti: Site_2: Xhol: mRNA was purified from embryonic
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CDNA 5., mRNA sequence.
A1353952
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Eukaryota: Metazoa; Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mahdiras.3.0., Wallace.J.C., Smith.K., Swartzell,S., Holzman,T.,
Rellet,A., Staker,K., Pirlong,J., Young,J., Zhao,S., Adams,M.D. 6
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BACKWARD: 5' GACTCAATTGAAATTGAACTAAGGGCG
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AV95:274 Nori Satch unpublished GNA library of ryses stage embryo
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                                                                                                                                                                 Email: jwallacełu washington.eda
Johose are derived from the human HAC library FFC-11. For BAC
Library availability, please contact Pieter of John
(pieter/dejong.med.buffalo.eda). Clones may be allevased from
AFCPAC Resources (http://bacpac.med.buffalo.eda). Affach
of from Resear Benelics (intofresquicom), HAC end Web Server:
http://www.htsc.washington.edu
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96 (17), 9739-9744 (1953)
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                                                           High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, KA 98709.
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Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satch
Department of Zoology
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Location/Qualifiers
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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Clark, M. Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, S., Hillier, L., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Washu Zebiafish EST Project 1998
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gil2224479|gb,AA455487|AA495487 fa09h12.rl Zebratish ICRFzfls Danio
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Actinopteryqii; Neopteryqii; Teleostei; Ostariophysi; Cypriniformes
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REDUCTASE COMPLEX CORE PROTEIN 2 PRECURSOR ;, mRNA sequence.
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Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems. St. Louis,
Missouri (web address: www.genomesystems.com) (enail contact:
infosteromicsystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resqen.com) (email contact: infosteromicsystems.com) and and desearch Genetics.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MC 63108, USA
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                                                                                                                                                                                                                                                                                Length 546;
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/tissue_type-"whole animal"
/dev_stage="cleavage stage embryo"
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52;
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Fax: 314-285-1810
Email: zbrafish<sup>dw</sup>atson.wustl.edu
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double-stranded chark was located 1. Suff. Ladgebors (PRE), digested with Not 1 and bloom 1 beto 15 Not 1 and Suff. Ladgebors transfer of the pSP-RE) vector (PRE). The research was mass to red by Matthew Clark (Debrach 126 TPE). The research Mass Planck Institut. There Modern are decret a fection, and was not bloodbemically naturalised. The research of the researc
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Washington University School of Medicine
4444 Ferest Park Parkway, Box 8501, St. Len. St. P. 64158
Tel: 814 286 1800
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Clark, M., Johnson, S.L., ichrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Myle, T., Underwood, K., Steptoo, M., Thensira, B., Alben, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, B., Harvey, N., Schurk, R., Ritter, F., Sohn, S., Shiz, L., Jackson, Y., Cardenas, M., McCann, R., Materston, R., and Wilson, R.
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reversed clone: similarity on wrong strand
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Matthew Clark, UNA Sequencing by: Washington University Genome
Sequencing Center Flone distribution: Genome Systems, St. Louis.
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4444 Forest Fark Parkway, Box 8501, St. Louis, MO 63106, USA
Tel: 414-286 1896
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DB 9; Length 618; 53;
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unpublished (1998)
Contact: Stephen is Johnson
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Email: chrafish@watson.wastl.edu
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Institut fuer Molekulare Genetik, Berith, CDNAS for EST analysis were selected following of genet-cotide hybridization fingerprinting of arrayed clones from zebrafish late Somitogenesis (26 ss), admit liver or embryonic shield stage (5.6 h) libraties. Fingerprint data were used to computationally cluster cDNAS, and a single CDNA from each cluster was chosen for sequencial in some cases multiple members of the same citater were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV997283 Nori Satoh unpublished CDNA library. Thaware stage embryo Cicoa intestinalis cDNA clone crol41114 57, skNA starvice. AV997283
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Eukaryota: Metazoa; Chorduta: Urochordata: Ascidiarea; Entercanna;
Phebobranchia: Cionidae; Ciona.
1 (bases 1 to 694)
Satoli, N., Satou, Y., Kohara, Y. and Shini, I.
Expressed genes in Ciona intestinalis
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Location/Qualitiers
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Pred. No. 54;
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Jel: 81-75-753-4081
Fax: 81-75-705-1113
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Department of Zoology
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CONA Library Picparation: Ling Hong/Rubin Laboratory
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inoyte Genomics, Inc.
Clone distribution: MGC clone distribution information ca: be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiCMIN 32 row: I column: 24
High quality sequence stop: 591.
Location/Qualifiers
I. 704
Arref-"Homo Sapiens"

// Ab_xref-"Homo Sapiens"
                                                                 Homo Sapiens
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: EuteleosLomi;
Mammalia: Eutheria: Primates: Catarrhini; Hominidae: Homo.
                                                                                                            Mammadian to 700)

NIH-MGC http://mqc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cqapbs r@mail.nih.gov
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/clone_lib="NIH_MGC_42"
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Job time : 3585 secs
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BI160520.1
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JOURNAL
COMMENT
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                                                                 ORGANISM
                                                                                                                   REFERENCE
AUTHORS
 ACCESSION
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                              KEYWORDS
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159
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/ cgn2_6/ptodata//lina/5A_COMB.seq:*

/ cgn2_6/ptodata//lina/5A_COMB.seq:*

/ cgn2_6/ptodata//lina/6A_COMB.seq:*

/ cgn2_6/ptodata//lina/6B_COMB.seq:*

/ cgn2_6/ptodata//lina/pcTUS_COMB.seq:*

/ cgn2_6/ptodata//lina/pcTUS_COMB.seq:*

/ cgn2_6/ptodata//lina/backfiles1.seq:*
GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen ...d.
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                                                                                                                                                                                                                                                                                                                                                                                                                    441362 segs, 153338381 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                              OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                Scoring table:
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## SUMMARIES

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Q	Score	Match	Length	DВ	ID	Les Sociption
	91	11.9	577	4	US-09-615-152A-97	Apply Apply Apply
?	19	11.9	624	~	US-08-713-000-9	ر ان
æ	75	11.9	624	~	US-08-975-316-9	2
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5	19	11.9	624	ಶ	US-09-615-192A-9	Sequence 9, Appli
2	19	11.9	684	7	US-08-975-316-45	Sequence 45, Appl
7	19	11.9	684	4	US-09-615-192A-45	<del>.</del> 5
ಹ ಬ	16	10.1	39	7	US-08-519-777-53	63,
σ. υ	16	10.1	39	_	US-08-742-035-63	63,
c 10	16	10.1	39	-	US-08-777-019 63	63,
· 11	16	10.1	39	~	US-08-777-143-63	53,
0 12	16	10.1	39	٣	US-08-775-414-63	83
c 13	16	10.1	39	4	US-08-931:858E-63	Sequence 63, Appl
÷1 0	9:	10.1	39	4	US-08-981-739-63	63,
c 15	16	10.1	39	4	US-09-128-026-63	63,
91 0	16	10.1	57	-	US-08-519-777-18	18,
C 17	15	10.1	57	-	US-08-742-035-18	Sequence 18, Appl
C 18	16	10.1	57	-	US-08-777-019-18	18.
c 19	16	10.1	57	7	US-08-777-143-18	Sequence 18, Appl
c 20	16	10.1	57	~	US-08-775-414-18	.8
c 21	16	10.1	57	4	US-08-931-858E-18	18,
c 25	16	10.1	57	4	US-08-981-739-18	18,
c 23	16	10.1	57	4	US-09-128-026-18	œ
c 24	16	10.1	169	~	US-08-519-777-29	58,
c 25	16	10.1	169	٦,	US-08-742-035-29	29,
د 36	16	10.1	169	-	-08-777-01	5.7
c 27	15	10.1	169	~	US-08-777-143-29	Sequence 29, Appl

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16   10.1   169   3   US-     16   10.1   169   3   US-     16   10.1   169   4   US-     16   10.1   169   4   US-     16   10.1   169   4   US-     16   10.1   285   1   US-     16   10.1   285   4   US-     17   10   10   10     18   10   10   10     10   10   10     10   10	PLLC , Suite
16	oicard P Avenue,
16   10.1   169     16   10.1   169     16   10.1   169     16   10.1   169     16   10.1   169     16   10.1   169     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     16   10.1   285     17   10.1     18   10.1   10.1     10   10   10     10   10   10     10   10	5 Pica Ave
16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     16   10.1     17   10.1     18   10.1     18   10.1     19   10.1     10   10     10   10     10   10     10   10	QUENCES: 15 CE ADDRESS: Speckman P 601 Elliott ttle
16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   16   10   10	ENC Spe Spe 12 E
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INFORMATION FOR SEU ID NO:
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                                                                                                                                                 Query Match
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TITLE OF INVENTION: MATERIALS AND METHOUS FOR
TITLE OF INVENTION: THE MODIFICATION OF SCANLICLINGS
NUMHER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, ! 1kk.
                                                                MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COERATING SYSTEM: PC-DOS/MS-LOS
SOFTWARE: PatentIn Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O8/713,000
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COMPRESSIONNEMS ADDRESS:
ANDHESSEE: LAW OITICES OF AND W. Specker in
STREET: 2601 Ellhott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11000/160301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILLING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/08975316
Patent No. 5952486
                                                                                                                                                                                                                                                       REGISSTRATION NUMBER: 37,007
REFERENCE/TOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
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FILECOMMUNICATION INFORMATION: 206-265-5
TELEFAX: 206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 actionerstached 279
                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 GITGGGIGTGGCTGAG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                                                                                                                                                                                                                                                                  : 206-269-0565
206-269-0563
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 624 base pairs
TYPE: nucleacid
STRANDEDNESS: single
TYPEAGY: linear
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Matches 19: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COM-
OPERATING SYSTEM:
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                                                                                                                                                                                     FILING DATE:
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                                 98121
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               COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-975 316-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bloksherg, Leonard N. APPLICANT: Havakkaig, likka APPLICANT: Havakkaig, likka IITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin Content CILE REPRENCE: 11009.1003.404
CURRENT APPLICATION UNRER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havikkaia, 11kka
APPLICANT: Havikkaia, 11kka
APPLICANT: Griesron, Alastair
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 1000-1003cs
CURRENT APPLICATION NUMBER: 105/09/211,710A
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0.64;
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100.0%; Pred. No. 0.6
.ive 0; Mismatches
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NUMBER OF SEQ ID NOS: 405
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: :5
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Sequence 9, Application 05/09211710A
; Patent No. 6204434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Sequence 9, Application US/096:5192A
: Patent No. 6410718
: GENERAL INFORMATION:
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100.0%; Fr.
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261 GCTGGGGGGGGTGGGGGAG 279
SEQUENCE CHARACTERISTICS:
LENGTH: 624 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                            70 GCTGGGCGTGCTGGAG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 GCTGGGGGTGTGTTGAG 88
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Matches 19; Conservative
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US-09-211-710-9
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3.3. 1987. 1. 1. 1887. 1. 1. 1887. 838
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                                  11.9%, Score 19; DB 4; Legath 52; 100.0%; Pred, No. 6.64; Ci. 1ndels.ive 0; Mismatches G; Indels.
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APPLICANT: Bloksberg, Leonard N.
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TTTLE -F INVENTION: Materials and Methods Desire
ITTLE -F INVENTION: Modification of Plant esquie ection:
FILE REFERENCE: 11000.1003e40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette CumpuTER: IRM Compatible OPERALING SYSTEM: BOS SOFTWARE: FastSDO for Windows Version 2.0 CURREN: APPLICATION DATA:

APPLICATION NUMBER: US/08/975,316
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PRICE APPLICATION DATA
APPLICATION NUMBER: 08/715,000
FILING DATE: SEPTEMBER: 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US (99 61% 1928-45
: Sequence 45, Application US/09615192A
: Patest No. 6416718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : Sequence 45, Application US/08975316
: Falent No. 5952486
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ TO NO: 45: SEGLENCE CHARACTERISTICS: LENSTH: 684 base pairs IYPE: nucleic acid STRANDENESS: single GEOMAGNASY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: SLEATH, Janet REGISTRATION NUMBER: 37,007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENTADOCKET NUMBER: 11
FELECAMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
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East Local Similarity Tourself the Stranger of 19: Conservative
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98:21
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08 08 575 316-45
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US-08 975 416 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [18] [K. Schreffel DB 1; Length 39;
[18,080 [1864] No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSE: ROJEKS, HOWELL & HAFERKAMP, L.C. STREEJ: 7734 PORKYJH RODLEVARD, SUITE 1400
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                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US UB/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 405
SOFTWAKE: FASLSEQ FOR WINDOWS Version 3.0
CURRENT APPLICATION NUMBER: US/09/515,192A CURRENT FILING OATE: 2000-07-12 PAPLICATION UNMESS: US 08/975,316 PRIOR FILING DAIR: 1997-11-21
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REPERENCE/DOUNCE NUMBER: 953095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Sequence 63, Application US/08519777 ; Patent No. 5739307
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100.0%; Pro
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity (100.)
Matches 19; Conservative
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INFORMATION FOR SEQ 1D NOT
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STRANDEDNESS: single
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CITY: ST. LAUIS
STATE: MISSOURI
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APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBEANFY: GEFFREY D.
APPLICANT: MILBEANFY: GEFFREY D.
APPLICANT: MILBEANFY: DAIL T.
APPLICANT: LAMPE, PATRICIA A.
TILLE OF INVENTION: NEUKTURIN AND RELATED GROWTH FACTORS
NUMBER OF SEQUENCES: 78
CORRESPONDENCE AUDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.1%; Score 16; DB 1; Length 39; 100.0%; Pred. No. 22; Use 0; Mismatches 0; Indels
                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWAKE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/777,019
FILING DATE: 40-DEC-1996
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FILING DATE: 30-DEY-1996
                                             COUNTRY: US
ZIP: 63.05 1817
COMPUTER REAGABLE FORM:
MEDIUM TYPE: FIGEPRY GISK
COMPUTER: 18M PC COMPATIBLE
OPERATING SYSTEM: PC-DAS/MS-DAS
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                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DAIA:
APPLICATION NUMBER: 08/519,777
FILING DATE: 28 AUG-1995
ATTORNEY/AGENT INFORMATION:
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ATTORNEY/AGENT INFORMALLING
                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 35.197
REFERENCE/DOCKET NUMBER: 95.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 7.27-5188
TELEFAX: (314) 7.27-5188
INFORMATION FOR SEC. ID NO: 64:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 AGENT INFORMALD R. HOLLAND, DONALD R. T. WIMBER: 35,197
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 39 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
US-08-777-019-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
       ST. LOUIS
MISSOURI
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CITY: ST. LOUIS
STATE: MISSOUR:
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63105-1817
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                                                                                                                                                                                                                                                                                                                                                                                           NAME:
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                                                                                                                                                                                                APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MILBRANDT JEFFREY D.
APPLICANT: KOTZBAUER, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
TIFLE OF INVENTION: NEURTURIN AND RELATED GROWIH FAULTSY
UNBERG OF SCOUNCES: 78
COMPRESSIVATIONE ADDRESS:
ALDRESSEE: ROGERS, HOMELL & HAFERKAMP, L.C.
STREET: 7734 FORSYTH BOULEVARD, SUITE 1406
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CHRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
computer: EM PC compatible
GERATURS SYSTEM: PC-ODS/MS-TXS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,035
FILING DATE: 01-NOV-1996
GLASSIFICATION: 435
FILING DATE: 01-NOV-1996
GLASSIFICATION: 435
FILING DATE: 28-AUG-1995
AILONALMANER: 28-AUG-1995
AILONALMANER: 28-AUG-1995
AILONALMANERATION:
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STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: HOLLAND, DONALD R.
RECISTRATION NUMBER: 35.197
REFERENCE/DOCKET NUMBER: 95.3095
TELEFOMMUNICATION INFORMATION:
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-5188
TELEFAX: (314) 727-6092
INPURMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: JOHNSON JR., EUGENE M. A: PLICANT: MILBRANDT, JEFFREY D. APPLICANT: KOTZBAUER, PAUL T. AFPLICANT: LAMPE, PATRICIA A.
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Parent No. 5817622
GENERAL INFORMATION:
                                                                                                                                    : Sequence 63, Application US/08742035
: Patent No. 5747655
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11 HILLHITHITH 55 GGCGGCTGCCAG 21
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STRANDEDNESS: sing)
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0S 68-742 035-63
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Matches 16; Conserv
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                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                        US-08-742 035-63/c
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; Snore 16; 08 %; Letitli %;
100.0%; Pred, No. 22;
Live 0; Mismatches C; Ind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: HOWELL & HAPERKAMP, L.C.
7733 FORSYTH BOULEVARD, SUITE 1400
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100.0%; Fred. No. 22.
110.0%; Freds. No. 22.
REGISTRATION NUMBER: 35,197
REFERENCE/ODCKET NUMBER: 953095
IELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 63:
SEGGEMER CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UMBER: US/08/775,414
31-DEC-1996
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APPLICANT: JOHNSON JR., EUGENE M.
APPLICANT: MICHANDT, JEFFREY O.
APPLICANT: MICHANDE, PAUL T.
APPLICANT: LAMPE, PATRICIA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 65, Application US/08775414 Patent No. 6090778
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REGISTRATION NUMBER: 35,197
REFERENCE/TOKET UNMBER: 96.58
REILFOWNENCE/TOKET UNMBER: 96.58
TELLEPHONE: (314) 727-5188
TELLEPHONE: (314) 727-6092
INFORMATION FOR SEQ ID NO: 63:
SEGUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.19
Best Local Similarity 100.6
Matches 16, Conservative
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EDNESS: single
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                          : MOLECULE TYPE: CDNA
US 08-777-143-63
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MOLECULE TYPE: CDNA
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STATE: MISSOURI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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US-08-775 414-53/C
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MILBRANDT, JEFREY D.
MOTIBAUER, PAUL T.
JAMPE, FATRICIA A.
TILLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS
NUMBER OF SQUENCES: 176
CORRESPONDENTE AUDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 39;
22;
                                                                                                                                                  APPLICANT: LAMPE, PATRICIA A
APPLICANT: KLEIN, KOHERT
APPLICANT: DESAUVAGE, FRED
ATTLE OF INVENTION: PERSPHIN AND RELATED GROWTH FACTOR
NUMBER OF SROUENCES: 239
CORRESPONDENCE ADDRESS:
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STREET: 7733 FORSYTH BOOLEVARD, SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/931,858E
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STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
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100.0%; Pred. No.
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OPERATING SYSTEM: PC-DOS/MS-180S
                           Sequence 63, Application US/08931858E
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| Sequence 63, Application US/08981739
| Patent No. 6232449
| GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: HOLLAND, DONALD R. REDISTRATION NUMBER: 45,197 REFERENCE/KONNET NUMBER: 971 TELECOMMUNICATION INFORMATION: 314-727-5188
                                                                                     APPLICANT: JOHNSON, EUGENE M
APPLICANT: MILBRANDT, JEFFREY
APPLICANT: KOTZHAUER, PAUL T
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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LENGTH: 39 base pairs
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INFORMATION FOR SEQ ID NO:
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STATE: MISSOURI
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STRANDEDNESS: single
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US-08-931-858E-63
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Best Local Similarity
Matches 16: Conserv
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                                          Patent No. 6222022
GENERAL INFORMATION:
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US-08-931-858E-63/C
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CHAPTER READABLE FORM:

MEDIUM TYPER FLORPY disk

MEDIUM TYPER FLORPY disk

CHAPTINE SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.6, V-1510B. Kl...

CHAPTING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.6, V-1510B. Kl...

APPLICATION NUMBER: OS/08/981.739

FILING DATE: 31-Aug-1998

FILING DATE: ALONGOWN-

PRICATION NUMBER: PCT/3057/0346.

FILING DATE: CORNOWN-

APPLICATION NUMBER: PCT/3057/0346.

FILING DATE: CORNOWN-

NAME: HOLLMON, DONALD R.

NAME: HOLLMON, DONALD R.

REFERENCE/DOCKET NUMBER: 97616.

TELEPRONE: (314) 727-5188

TELEFAX: (314) 727-5188
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Live 0; Mismatches 0; notels
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APPLICAN: MILBRANDI, JEFEREY D.
APPLICAN: MILBRANDI, JEFEREY D.
APPLICAN: ACCESABLER, PAUL T.
ALPLICAN: LAMPE, BATRICIA A.
TITLE OF INVENTION: PERSEPHIN AND RELATED DRING.
NUMBER OF SEQUIRNCES: 176
APPRESENT ADDRESS:
ARREST: MOMECLE ADDRESS:
ARREST: AT33 FORSYTH BOULEVARD, SUITE LACO
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OPERATING SYSTEM: PC-DOS/MS-164S
SOFTWARE: Patentin Release #1.0, Vetsion #1.1
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SEQUENCE DESCRIPTION: SEQ 10 NO: 63:
OS:08+981-739-63
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NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 97.197
REFERENCE/FOCKEI NUMBER: 976.163
TELEFROMSUNICATION (THOCHARTION:
TELEFROMSUNICATION (THOCHARTION:
TELEFROMSUNICATION (19.4) 727-5188
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APPLICATION NUMBER: US/09/128,026
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Sequence 6. A pulcation US/09128025
Catchel No. 640.835
General INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Loral Similarity 100.0
Matches 16. Conservative
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SITY: ST. LOUIS
SIATE: MISSOURI
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| INFORMATION FOR SEG IE NO: 63:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 39 base pairs |
| TYPE: nucleic acid |
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May 10, 2003, 02:15:59 ; Search time 124 Ser rus
(Without alternmen s)
1593.468 Million vii updates/sec
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159
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| Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.sev;:*
| Cqn2_6/ptodata/2/pubpna/PCT_WMS_PUB_Sev;:*
| Cqn2_6/ptodata/2/pubpna/BCT_WMS_PUB_Sev;:*
| Cqn2_6/ptodata/2/pubpna/US06_PUBCCMB.sev;:*
| Cqn2_6/ptodata/2/pubpna/US06_PUBCCMB.sev;:*
| Cqn2_6/ptodata/2/pubpna/US08_PUBCMB.sev;:*
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| Cqn2_6/ptodata/2/pubpna/US00_UBC_WBS_Sev;:*
| Cqn2_6/ptodata/2/pubpna/US60_UBW_PUBS_Sev;:*
| Cqn2_6/ptodata/2/pubpna/US60_PUBCCWB.sev;:*
GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compuger Ltd.
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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121 CIGCTETGGAAGAACCICACTITGAGAAGAAGAAGA 159

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Sequence 102, App Sequence 103, App Sequence 104, App Sequence 104, App Sequence 106, App Sequence 107, App Sequence 107, App Sequence 111, App Sequence 112, App Sequence 111, App Sequence 113, App Sequence 118, App Sequence 121, App Sequence 121	or the ABC1 Gene, Molecules Modif Uses	tch 100.0%; Score 159; DB 10; Length 159; al Similarity 100.0%; Pred. No. 8.1e-79; Indels 0: Gaps 0; 159; Conservative 0; Mismatches 0; Indels 0: Gaps 0; TTAATGACCAGGGGGTCCTGCTGTCTGGCGTGCTTCCAGGGCTTCCC 111111111111111111111111111111
9 0S-09-984-827-103 9 0S-09-984-827-104 9 0S-09-984-827-105 9 0S-09-984-827-105 9 0S-09-984-827-107 9 0S-09-984-827-107 9 0S-09-984-827-110 9 0S-09-984-827-110 9 0S-09-984-827-110 9 0S-09-984-827-111 9 0S-09-984-827-111 9 0S-09-984-827-111 9 0S-09-984-827-111 9 0S-09-984-827-111 9 0S-09-984-827-111 9 0S-09-984-827-111 9 0S-09-984-827-115 9 0S-09-984-827-116 9 0S-09-984-827-112 9 0S-09-984-827-112 9 0S-09-984-827-112 9 0S-09-984-827-122 9 0S-09-984-827-122 9 0S-09-984-827-123 9 0S-09-984-827-123 9 0S-09-984-827-123 9 0S-09-984-827-123 9 0S-09-984-827-123 9 0S-09-984-827-123 9 0S-09-984-827-123	ENTS Acid for peutic	tch 100.0%; Score 159; DB 10; Length 159; al Similarity 100.0%; Pred. No. 8.1e-79; Indels 0: G 159; Conservative 0; Mismatches 0; Indels 0: G TTAATGACCAGGCGTCCTGCTGTCAGCCGTGCCTTCCAGGCCTTCCAGGCCTTCTTCTCCTTTTTTTT
66 37.7 9870 66 37.7 9870 66 37.7 9870 66 37.7 9870 66 37.7 9870 66 37.7 9870 66 37.7 9870 67 37.7 9870 68 37.7 9870 69 37.7 9870 60 37.7 9870	RESULT 1  US-09-846 456-5  Sequence 5, Application US/09846456  Sequence 5, Application US/09846456  Sequence 5, Application US/09846456  Sequence 5, Application US/09846456  Setent No. USSOUSDULATION  APPLICANT: Prades, Carberine  APPLICANT: Denefic, Parrice  APPLICANT: Denefic, Parrice  APPLICANT: Denefic, Parrice  APPLICANT: Denefic, Parrice  APPLICANT: Brewer, Bryan  APPLICANT: Brewer, Bryan  APPLICANT: Ecolo, Silvia  IITLE OF INVENTION: Regulatory Nucleic  IITLE OF INVENTION: Regulatory Nucleic  CURRENT FILING DATE: 2000-05-02  PRIOR TING DATE: 2000-05-02  PRIOR FILING DATE: 2000-05-02  PRIOR FILING DATE: 2000-05-02  PRIOR FILING DATE: 2000-05-02  SOUTHARE: PATENTION NUMBER: US 60/201, 28G  PRIOR FILING DATE: 2000-05-02  SEC ID NO 5  LENGTH: 159  LENGTH: 159  LENGTH: 159  CORGANISM: Homo Sapiens	Match Local Similarity 100 les 159; Conservative 1 TTAATGACCAGCGGGG 1 ITTAATGACCAGCGGGGGGGGGGGGGGGGGGGGGGGGGGG
01222222222222222222222222222222222222	RESULT 1 US-09-846-456 Sequence 5, Sequence 5, Setent L INF APPLICANT: BRIOR FILLI	Ouery Matc Best Local Matches 1 Qy 1 TT Db 1 TT

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APELICANT: DENEFLE, PATRICE
APELICANT: ROSIER-MCNIUS, MARIE-FRANCOISE
APPLICANT: ROSIER-MCNIUS, MARIE-FRANCOISE
APPLICANT: ARNOULD REGUIGNE, ISABELLE
APPLICANT: CAMRIEN, FRANCOIS
ITTLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARCAL GENE, INSIR USES, TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARCAL GENE, INSIR USES, FILE REFERENCE: 03856.0522 00000
CORRENT APPLICATION NUMBER: US/09/944.827
CORRENT APPLICATION NUMBER: US/09/944.827
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                                                                                                                                          100.0%; Score 159; DB 10; 100.0%; Pred. No. 7.9e-79;
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100.0%; Pred. No. 6.5e-70;
tive 0; Mismatches 0;
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APPLICANT: POSITS MONIUS, MARIE FRANCHISE
APPLICANT: ARMAGIL RESULANE, ISABELLE
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PRIOR FILING DAIE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ 1D NUS: 161
SOFTWAKE: Patentin Vel. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/09984827 publication No. US20030056234A1 GENERAL INFORMATION:
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                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 159; Conservative
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Matches 143; Conservative
; TYPE: DNA
; ORGANISM: Homo sapiens
US-69-846-456-2
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08-09-984-827-25
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APPLICANT: ROSIEM-MONIUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-RECUIGNE, ISABELE
APPLICANT: ARNOULD-RECUIGNE, ISABELE
APPLICANT: ARNOULD-RECUIGNE, ISABELE
APPLICANT: ARNOULD-RECUIGNE, ISABELE
APPLICANT: CAMBIRN, FRANCOIS
APPLICANT: CAMBIRN, FRANCOIS
TITLE OF INVENTION: DETECTION WETHOOS AND KITS THEREPOR
FILLS REFERENCE: 03806.0522-00000
CUCHENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2000-12-11
PRICH FILING DATE: 2000-12-11
PRICH FILING DATE: 2000-12-11
PRICH FILING DATE: 2000-10-31
NUMBER OF SEV ID NOS: 161
SWITWARE: PATENTIN VET: 2.1
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   Sequence 4, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
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Patent No. US2020146792Al
: GENERAL INFORMATION:
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APPLICANT: Lemoine, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
APPLICANT: Denefle, Patrice
APPLICANT: Buverger, Nicolas
APPLICANT: Brewer, Bryan
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69-984-827-4
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US-09-984 827 4
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37,7%: Score 60; DB 9; Lv 100,0%; Pred. No. 9,6e-24; 100.0%; Pred. wc.

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Best Local Similarity 100.0
Matches 60: Conservative
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    APPLICATE CAMBLEN, FRANCOIS
FITLE 04 INVENTION: POLYMORPHIC SEQUENCES 05 THE HOMAN ALONG SENE, THEIR USES, AND FITLE 04 INVENTION: POLYMORPHIC SEQUENCES 05 THE HOMAN ALONG SENE, THEIR USES, AND FITLE 04 INVENTION: DETECTION METHODS AND KITS THEREFORE CHURENTED 30806 0552-000000 AND KITS THEREFORE CHURENTED APPLICATION NUMBER: US/094,827 CHURENT FITNS DATE: 2002-04-03 PRIOR APPLICATION NUMBER: 2002-04-03 PRIOR APPLICATION NUMBER: FR US/14037 PRIOR APPLICATION NUMBER: FR US/14037 PRIOR FILMS DATE: 2000-12-11 PRIOR FILMS DATE: 2000-10-31 SIGNIBLE OF SEQ 10 NGS: 161
SSOFTWARE: PALCIALLY VEY: 2.1
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APPLITANT: Tanaka, Hitoaki
TITLE OF INVENTION: HUMAN CONAS AND PROTEINS AND ISLS THERE S
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Publication No. US20030027248A1
GENERAL INFORMATION:
DUVERGER, NICOLAS
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; OKGANISM: Homo sapiens
US-09-984-627-26
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LOPACTON: 154..639
NAMEZKEY: 3°CTR
LOKACTON: 640..1062
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1347..1062
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LOCATION: 1...153
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LENGTH: 159
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APPLICANT: Tacks, ilroaki
TITLE OF INVENTION: ilmonk constant proteins and USES THEREOF
FILE REFERENCE: 91.034.Div
CORRENT PAPPLICATION NUMBER: US/09/992.600A
CURRENT FILING DATE: 2001-11.13
PRIOR APPLICATION NUMBER: US 09/924.340
PRIOR APPLICATION NUMBER: US 06/924.340
PRIOR APPLICATION NUMBER: US 60/302.277
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-03-06
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-06-19
PRIOR PRILING DATE: 2001-06-19
PRIOR PRILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/298.698
PRIOR APPLICATION NUMBER: US 60/298.574
PRIOR APPLICATION NUMBER: US 60/298.598
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/298.574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/298.574
PRIOR FILING DATE: 2001-06-25
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AD (CAM) (CAS) IN BOARDS, BARDE FRANCOUSE
ABOUT (CAM) (ASK U. C. FLO CAS) (SABEL USA)
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publication No. US20030527361Al
GENERAL INFORMATION:

    Sequence L. Application USZ andez?
    Lotinalia No. PSZ condition.
    GENERAL INFORMATIN.

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NAME/KEY: CLS
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US 09-992-600A:101
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NAME/KEY:
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APPLICANT: BENEFIE, FATRICE
APPLICANT: RUSIER MONUS, MARIE-FRANÇOISE
APPLICANT: ARNOLID-REGUIGNE, ISABELLE
APPLICANT: ARNOLID-REGUIGNE, ISABELLE
APPLICANT: CAMBLEN, FRANCOIS
APPLICANT: CAMBLEN, FRANCOIS
TITLE DE INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, TITLE OF INVENTION: DEFERTION METHODS AND KITS THERFOR
FILE REFERENCE: 04806.0522-00000
FILE REFERENCE: 04806.0522-00000
FILE REFERENCE: 04806.0522-00000
FILE REFERENCE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254.108
PRIOR APPLICATION NUMBER: FR U0/14037
PRIOR APPLICATION NUMBER: FR U0/14037
PRIOR APPLICATION NUMBER: FR U0/14037
PRIOR FILING DAIE: 2000-10-31
NUMBER: OF SEQUENCE: 2000-10-31
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Publication VUS2036056234A1
GENERAL INFORMATION:
APPLICANT: DENEFLE, PATRICE
APPLICANT: ASSIEK WANTUS, MAKIE-FRANCOISE
APPLICANT: ANONUD-REGUIGNE, ISABELLE
APPLICANT: ANONUD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: DOVERGER, NICOLAS
APPLICANT: DOVERGER, NICOLAS
APPLICANT: DOVERGER, NICOLAS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, FHEIR USES, FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09984,827
CURRENT PILING DATE: 2002-04-01
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9e-24;
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Pred. No.
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PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
                                            Sequence 92, Application 0S/09984827
Publication No. 0S20030056234Al
GENERAL INFORMATION:
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US-09-984-827-92
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Matches 60; Conservative
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SEQ ID NO 93
LENGTH: 9870
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LOCATION: (7138)
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Best Local Similarity
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SEQ ID NO 92
                    US-09-984-827-92
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) OTHER INFORMATION: "n" is chosen from q, a, t and c
US-09-846.456-10
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Hest Excal Similarity 100.0%; Pred. No. 9c.24;
Matches 60; Conservative 0; Mismatches (
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Fatent No. US20020146792A1
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US-09-984-827-1
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APPLICANT: Prades, Catherine
APPLICANT: Lemoine, Cendrine
APPLICANT: Naudin, Laurent
APPLICANT: Denetle, Patrice
APPLICANT: Buverger, Nicolas
APPLICANT: Remaley, Alan
APPLICANT: Remaley, Alan
APPLICANT: Folo, Silvia
APPLICANT: DUVERGER, NICOLAS
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified_base
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           LENGTH: 9741
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US-09-846-456-10
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NAME/KEY: modified_base // LOCATION: (7138) // OTHER INFORMATION: 4, t, c or g US-09-984-827-95
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                                                                                                             Query Match
Best Local Similarity
Matches 60: Conserv
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APPLICANT: MEDEMELLS, MARIE-FEANCOISE
APPLICANT: MESSIER-MONIUS, MARIE-FEANCOISE
APPLICANT: MESSIER-MONIUS, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, SEQUENCES OF THE HUMAN AH-AL GENE, THEIR USES, AND
ITLE OF INVENTION: DETECTION METHODS AND KITS THERFOR
FILE MEFERING: 03806.0522-0000
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR APPLICATION NUMBER: FR 00/14037
NUMBER: CALCALL OF SECUENCES
SOFT WAREH
SEQ ID NOS: 161
SEQ ID NO 94
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APPLICANT: ROSIER-MONTUS, MARIE FRANCOISE
APPLICANT: AKNOULD-REQUIGNE, 1SABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN APPLICANT THE OF INVENTION: DETECTION METHODS AND KITS THEREFUR
      Saps
         0: Gaps
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         Inde. s
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      Mismatches
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CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIGH APPLICATION NUMBER: 60/254,108
PRIGH APPLICATION NUMBER: FR 00/14037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 95, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
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Publication No. US20030056234A1
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Rest Local Similarity 100.0%; P
Matches 60; Conservative 0;
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      60; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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      Matches
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APPLICANT: DENEFLE, PATRICE
APPLICANT: BOSIER MONULOS, MARIE-FRANCOISE
APPLICANT: ROSIER MONULOS, MARIE-FRANCOISE
APPLICANT: ARMOULO, REGULGE, ISABELLE
APPLICANT: CARMULON-REGULGE, NICOLAS
APPLICANT: CAMBIEN. FRANCOIS
TILLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
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APPLICANT: BOSIEK-MONTOS, MANIE-FRANCOISE
APPLICANT: ROSIEK-MONTOS, MANIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DOVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL SENE, THEIR USES, A
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
FILE REFERENCE: 03806.0522-00000
FULCHERIT FILLING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
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Sequence 96, Application US/09984827
Publication No. US20303086234Al
GENERAL INFORMATION:
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GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.1
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APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNCOLD-REGUIGNE, ISABELLE
APPLICANT: DUVECER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
TITLE (F. INVENTION: POLYMORPHIC SECUENTES (F. THE HEAN ASSYLETTE (F. INVENTION: DEFECTION WETHORS AND KITS TRUSTED (THE PETER PETER PETER PATRICATION NUMBER: US/09/784. dz)
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APPLICANT: ROSIER-MONIUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: ANNOULD-REGUIGNE, ISABELLE
APPLICANT: OVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TILLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUM
TILLE OF INVENTION: POLYMORPHIC METHODS AND KITS THER
FILE REFERENCE: 03806.0522-0000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT APPLICATION NUMBER: 60/224,108
PRIOR PELLING DATE: 2000-12-11
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PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID M.S.: 161
SOFTWARE: Patentin Ver. 2.1
                              Sequence 158, Application US/9984827
Publication No. US20030056234Al
GENERAL INFORMATION:
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APPLICANT: RANOULD-REGUIGNE, ISABÉLLE
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APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, PRANCOIS
APPLICANT: CAMBIEN, PRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, TITLE OF INVENTION: DELECTION METHODS AND KITS THEREFOR FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CGRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR APPLICATION NUMBER: EN 00/14037
PRIOR APPLICATION NUMBER: FR 00/14037
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APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ANOUGH REGOIGNE, ISABELLE
APPLICANT: ANOUGH REGOIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HOMAN APPLICANT OF INVENTION: POLYMORPHIC SEQUENCES OF THE HOMAN APPLICANT OF INVENTION: DOLYMORPHIC SEQUENCES OF THE HOMAN APPLICANT ON OWNER: US/09/944,827
CURRENT APPLICATION NUMBER: US/09/944,827
CURRENT FILLNG DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
FRICK FILLNG DATE: 2000-12-11
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Smilarity 100.0%; Pred, No. 3;
42; Conservative 0; Mismatches 1;
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NUMBER OF SEQ JU NOS: 161
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: DENSITE, MAKIE FRANCOISE

APPLICANT: ANONID, REGULGNE, ISABELLE
APPLICANT: ANNOID, REGULGNE, ISABELLE
APPLICANT: ANNOID, REGULGNE, ISABELLE
APPLICANT: CAMBREN, FRANCOIS
APPLICANT: CAMBREN, FRANCOIS
APPLICANT: CAMBREN, FRANCOIS
TITLE OF INVENTION: UDIFFICITION WETHOUS AND KITS THEREFOR
FILE OF INVENTION: UDIFFICITION WHOREN: US/09/984,827
CURRENT APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
SOFTHARE: Patentin Ver: 2.1
SEQ ID NO 141
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98.2%; Score 2842; DB 9; Length 2893;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2892; Conservative 0; Mismatches 1; Indels 0.
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Publication No. US20030056234Al
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-984-827-141
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APPLICANT: DENDELE, PATRICE
APPLICANT: BOSIER WOUTUS, MRIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGÜEK, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: PULYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, TITLE OF INVENTION: DEPLETION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: 05/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR APPLICATION NUMBER: FR 00/14037
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Sequence 144, Application US/09984827
Publication No. US20030056234A1
GENERAL INFORMATION:
APPLICANT: DENEFIE, PATRICE
APPLICANT: ROSIER-MONTUS, MARIE-FRAN
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APPLICANT: MOSTER-MONIUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: ANDUERGER, NICOLAS
APPLICANT: OUDVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
ITILE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NOWBER: US/09/984.827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 04/254,108
PRIOR APPLICATION NUMBER: FR 00/14037
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APPLICANT: DENEELE, PATRICE
APPLICANT: MCSIER-MONUS, MARIE-FRANCOISE
APPLICANT: ARNOILD-REGUIGNE, ISABELLE
APPLICANT: ARNOILD-REGUIGNE, ISABELLE
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: DOLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES, TITLE OF INVENTION: DEFECTION METHODS AND KITS THEREFOR FILE OF INVENTION: DEFECTION METHODS AND KITS THEREFOR CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-10-11
PRIOR FILING DATE: 2000-10-31
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Publication No. US20030056234Al
GENERAL INFORMATION:
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Sequence 153, Application US/09984827

Sequence 153, Application No. US20630056234a1

GENERAL INFORMATION:
APPLICANT: DENEFLE, FATRIC.
APPLICANT: DENEFLE, PATRIC.
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: CAMBTEN, FRANCOIS
TITLE OF INVENTION: DEFECTION METHODS AND KITS THEREFOR
TITLE OF INVENTION: DEFECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806,0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827

FILE REFERENCE: 03806,0522-00000
CURRENT APPLICATION NUMBER: FR 00/14037

PRIOR FILING DATE: 2000-10-31

NUMBER OF SEO ID NOS: 161

SOFTWAKE: PATELL 2000-10-31

NUMBER OF SEO ID NOS: 161

SSOTHARE: PATELL VON SEO ID NOS: 161

SSOTHARE: PATELL VON SEO ID NOS: 161

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APPLICANT: BOSIER-MONTGS. MARIE-FRANCOISE
APPLICANT: ROSIER-MONTGS. MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DOVERGER, NICOLAS
TOTTLE CF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABA'A] GENE, THEI
TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 03806.0522-00000
CURRENT APPLICATION NUMBER: US/09/984.P27
CURRENT FILING DATE: 2002-04-01
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
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Sequence 155, Application US/09984827
Publication No. US26030056234A1
GENERAL INFORMATION:
APPLICANT: DENEFLE, PATRICE
APPLICANT: ROSIER MONTUS, MARIE-FRANCOISE
APPLICANT: ROSIER MONTUS, MARIE-FRANCOISE
APPLICANT: PUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: FRANCOIS
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 FILE REFERENCE: 03806, 0522-00000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/254,108
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PRIOR APPLICATION NUMBER: 60/254,108
PRIOR PRICRET: 2000-12-11
PRIOR FILING DATE: 2000-12-11
SPRIOR FILING DATE: 2000-10-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver: 2.1
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Matches 2892; Conservative
                                                                                              TYPE: DNA ORGANISM: Homo sapiens
INVENTION:
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                                                                                                               US-09-984-827-155
                                                                                SEC ID NO 155
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RESULI 2: US-09-984-827-157

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APPLICANT: DENETLE, PATRICE
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APPLICANT: ROSIER MONTUS, MRRIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: DELYMORPHIC SEQUENCES OF THE HUMAN ABCA; GENE, THEIR USES,
TITLE OF INVENTION: DEPECTION METHODS AND KITS THEREFOR
TITLE OF INVENTION: DEPECTION METHODS AND KITS THEREFOR
CURRENT FILING DATE: 2000
CURRENT FILING DATE: 2000
PRIOR APPLICATION NUMBER: GV254,108
PRIOR FILING DATE: 2000:12-11
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR APPLICATION NUMBER: FR 00/14037
PRIOR FILING DATE: 2000:10-31
SPRIOR FILING DATE: 2000:10-31
NUMBER OF SEQ 1D NOS: 161
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Sequence 157, Application US/09984827 Publication No. US20030056234A1 GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 2892; Conservative
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US-09-984-827-157
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                                                                                                                                                 APPLICANT: BOSIER-WANTUS, MRIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: CAMBIEN, FRANCOIS
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CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-10-31
NUMBER OF SEV 1D NOS: 161
SOFTWARE PLEATION VET. 2.1
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Sequence 147, Application US/09984827
Publication No. US20030056234Al
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                       CGGCAAAACCCC 2893
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09:984:827:147
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LENGIH: 289
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Sequence 156, Application US/09984827

EDULICATION

GENERAL INFORMATION:

APPLICANT: BENEFLE, PAIRICE

APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

APPLICANT: ROSIER-MONTUS, MARIE-FRANCOISE

APPLICANT: ARNOULD-REGUIGNE, ISABELLE

APPLICANT: CAMBIEN, FRANCOIS

TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES,

ITILE OF INVENTION: DUMBER: US/09/984,827

CURRENT APPLICATION UNMBER: 60/254,108

PRIOR APPLICATION NUMBER: 60/254,108

PRIOR PILING DATE: 2000-12-11

PRIOR PELLING DATE: 2000-12-11

PRIOR FILING DATE: 2000-12-11

WUMBER OF SEQ ID NOS: 161

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Best Local Similarity 100.5
Matches 2670; Conservative
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                                                                                                                                                            SOFTWARE: Patentin Ver.
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US-09-984-827-156
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GGAGGAAGGAAGGAAGC 
CAGAGCAGAAAGACTT 
ACCCAATTTATTGACCA  :
CTTGGGCTTTAGAAAGCT 
TCTFGACACGGAGTCTTC 
ACTGTAACCTCTGCGTCC
GGCGCCGGCACCACATC TITITITITITITITI GGCGCCGCCACCACAT
GTTGGCCAGGTTGGTTTG 
AGTGCTGGGATTACAGGC 111111111111111111111111111111111
26] CTAAGGGCAAACAGTCCAFGGTGCAAAGGGGCCAFACCACCAGAGTTALAGTAGTTGG 132 
KGAATTCCTTGCCTGGTGG 
SCCTCTGTCCTGAGTGTTG 
GGAGATCCTGTTGACTGT 

2280 1980 2040 2160 2160 2220 2220 2280 2340 2340 2400 2400 2460 2460 2580 1560 1620 1620 1680 1680 1740 1800 1860 1860 1920 1920 1980 2040 2100 2100 252C 2520 1800 GTCCTGTGTTTTTTCACAGGGGGGCTGATGTATAATGAAATTAAAAGGGGGCTGGTC CACCCCAGCCTAGGCCTTTGAAAGGAAACAAAAGACAAGACAAAATGATTGGCGTCCTGA TGCAGGTGGTGGGAGTTCTGGAATATGATGGAGCTGGAGGTGGGAAGAAGAAGTAGGCTTG AATTIIACAGAGTGGAATTCTC1GGCTGCACTTCACAAATGTATACAAACTAAATACAA 4411 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 1444 : 14 GIGGCCTCCACGTGCACTTCCAGGGCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGT CCTGGGGGGGCTCVGGGGATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTC CAGGITTGTGGGGGGAAAAAAAAAAGCAGCCCAITACCCAGAGGACTGTCCGCTTCCCCT AAAGGAAAAAAAA HUGGGAAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCTT AAATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGCCTT CTICIATGAATCCTTCAGGGCAGATTCATATTTAGACTCTTCACAGTTTGACCTGAGTTT TGGTGTGTAGGCCTGCAT+CCTACTCTTGCCTTTTTTTTGCCCCTCCAGFGTTTTTGGGT AGTITIENTENNE I ANAKONAAAGO AAACAGAGAAGITGGAGICTGGAGIGGC TACAI 7161 2161 1741 2221 2281 2281 2341 2461 2461 1501 1501 1561 1561 1621 1621 1681 1681 1741 1801 1801 1861 1861 1921 1921 1981 1981 2041 2041 2221 2341 2401 2401 2521 a qq 2 q g 음 ò qq 0y qq ò S ò ò QQ ô ć ੜੇ Š 50 Ś ò QQ ŝ g ŝ E 5 5 g ò qq οy ô ò

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CCCAGCTACTTGGGAGGCTAAGGTGGGAGGATCGCTTGAGCCCAGGGAGTCAAGA
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APPLICANT: DENEFLE, PATRICE
APPLICANT: DENEFLE, PATRICE
APPLICANT: MOSIER-MONTUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REGUIGNE, ISABELLE
APPLICANT: DUVERGER, NICOLAS
APPLICANT: CAMBIEN, FRANCOIS
TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HU
FILLE HEFERENCE: 08806,0522-0000
CURRENT APPLICATION NUMBER: US/09/984,827
CURRENT PILING DATE: 2002-04-01
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR PPLICATION NUMBER: FR 00/14037
FRICH FILING DATE: 2000-10-31
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Pred. No. 0;
                                          2670
                                                    2641 CCTGCTGTACCTCCACCCACCCACCC 2670
                                          CCTGCTGTACCCTCCACCCCCACCCCACCC
                                                                                                                Sequence 150, Application US/09984827 Publication No. US20030056234A1 GENERAL INFORMATION:
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99.9%;
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SOFTWARE: PatentIn Ver. 2.1
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Matches 2889; Conservative
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                                                                                            RESOLT 24
US-09-984-827-150
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APPLICANT: ROSIEK MONIUS, MARIE-FRANCOISE
APPLICANT: ARNOULD-REQUIGNE, ISABELLE
APPLICANT: ARNOULD-REQUIGNE, ISABELLE
APPLICANT: ANGUERNER, NICOLAS
APPLICANT: CAMBREN, FRANCOIS
ITTLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES,
ITTLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ABCAL GENE, THEIR USES,
ITTLE OF INVENTION: DEFECTION METHODS AND KITS THEREFOR
FILE REFERENCE: 018046,0522-00000
CURRENT APPLICATION NUMBER: 60/254,108
PRIOR APPLICATION NUMBER: 60/254,108
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-13-11
NUMBER OF SEQ ID NOS: 161
2821 GCTTTGACUGATAGTAAQCTCTGGGCTGCGGTGCGAATCTATAAAAGGAACTAGTGC 2880
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                                                          AGATGGAGGGTCAGGGAGATCTAATTACTCTCTAAAATCATGCTAGGAAAGATAACACCT
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Pred. No. 0;
                                                                                                                                                                                                                                                                                ; Sequence 151, Application US/09984827
; Publication No. US20030056234Al
; GENERAL INFORMATION:
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99.7%;
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SEQ ID NO 151
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Best Local Similarity 99.7°
Matches 2884; Conservative
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US-09-984-827-151
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ć o	1621 1621	AAAIGEGAAICEGCCTECAAGGEGGCTACAAAGGTATCTTTGTCAAGGTAGGAGCCTT 1680 
co ob ob	1681 1681	GTGGCCTCCACGTGCACTTCCAGGCCTGCTTGGGCCTCTTCTACGGGTCTGTCCTGAGT 1740 [
č a	1741	CTICTATGAATCCIICAGGGGAGATTCATATTAGACTCTTCACAGTTTGACCTGAGTTT 1800
à a	1801	TGGCCAGAATAAGGTGACATTTAGTTTGTTGGCTTGATGGATG
λ a a	1861 1861	TGGTGTGTAGGCGGCTGCGTAGTGTTGCCTTTTTTTTGCCCCTCCAGTGTTTTGGGT 1920
ςς DP	1921	AGTITIGCICCCCIACAGCCAAAGGCAAACAGAGAAGTIGGAGGCTCTGGAGIGGCTACAT 1980
à a	1981	AATTTTACACGACTGCAATTGTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAA 2040
č da	2041	GTCCTGRGTITTTALCACAGGAGGCTGATCAATATAATGAAATTAAAAGGGGGTGGTC 2100 
λ a	2101	CATATTGIICTGTGTTTTTGIITGTTTGTTTGTTTGTTTGTTTTTTTT
λς Op	2161	ICCTTCCTCTCAATHATGAAGAAAGCAGTAAGATGTTCCTCTCGGGGTCCTCTGAGGA 2220 
cy Oge	2221	CCTGGGGAGCTI'AGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTC 2280 
oy Ob	2281	CAGGTITGTGGGGGAAAAAAAAGCAGCCATTACCCAGAGGACTGTCCGCCTTCCCCT 2340 FILLFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
λ O	2341	CACCCCAGCCTAGGCCTTTGAAAGGAACAAAAGACAAGACAAATGATTGGCGTCCTGA 2400 
λς op	2401	GGGAGATTCAGCCTAGAGCTCTCTCTCCCCAATCCCTCCC
င် င်	2461	AAAGGAAAAAAAAATTGCGGAAAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTT 2520 
ŝ	2521	GGCTGPGGGGAAGTGGACTAGAAGTCTGGGGGGGAGCCCGAGCCCAGCCTTCCCGC 2580

AACA 3 1111 3 AACA 3 1111 3 1111 3 1111 6 GAGG 4	421 481 481 541 541	Oy         601 CTGAGCCATGATTGGATCACTGCAGCCTGGGTAGACAGAGCACTGTCA 660           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy   771   AAAAAACAAAACAAAACAGAAAAGACTTTACGTAAATTGCTCATCATGTGGTTG   830   11111111111111111111111111111111111	QY   951 CCCTTCITTTALITTTCITGACACGAGTCTTGCTCTCTCACGCTGAGTGCAG 1010	Oy 1071 AGCCTCCTGAGATAACAGGCCCGCCACATCTGGCTAATTTTTGTATTTTTAGTAA 1130    11111111111111111111111111111111111
2512 idotracoggaaacgragacragacgacacacaccagacccaangccannicragaca 2511 2581 dcoretracoccacacacacacacacacacacacacacacacacac	2761 TGAGTGACTGAACTACATAAACAGAGGCCGGAAUGGGGCGGGGGGGGGG	-138 No. US2003 ORMATION: DENEFICE RNOULD-F DUVERGER.	TITLE OF INVENTION: POLYMORPHIC SEQUENCES OF THE HUMAN ARGAI GENE, THELR USES, AND TITLE OF INVENTION: DETECTION METHODS AND KITS THEREFOR CURRENCE: 03806.052-00000 METHODS AND KITS THEREFOR CURRENCE: 03806.052-00000 METHODS AND KITS THEREFOR CURRENCE: 03806.052-00000 METHODS AND KITS THEREFOR CURRENT APPLICATION NUMBER: 05/09/984,827 PRICHE FILING DATE: 2000-12-11 PRICHE APPLICATION NUMBER: FR 00/14037 PRICHE FILING DATE: 2000-12-11 PRICHE PRICHE PRICHE PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: PRICHES: 2000-10-31 NUMBER: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: PRICHES: 2000-10-31 NUMBER: 20	LENGTH: 2903  LENGTH: 2903  IYPE: DNA  ORGANISM: Homo sapiens  -09-984 827-138  77.2%: Score 2235; DB 9; Lengt: 2903;  Best Loral Similarity 99.7%; Pred. NO: 0:  Matches 2893; Conservative 0: Mismatches 0: Indo: N. 10: Gaps 1:	CONTROLLE CONTROLL CONTROL CONTROLL CONTROLL CONTROLL CONTROLL CONTROL CONTROL CONTROL CONTROL CONTROLL CONTROLL CONTROL CONTROL

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Publication No. US20030059875A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214C1
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Patent No. US/0020115171A1
GENERAL INCONATION
TOTAL OF INCONATION
TITLE OF INVENTION: INCLEIC ACID MOLECULES ENCODING
TITLE OF INVENTION: PROTEIN AND USES THEREOF
FILE REFERENCE: CLOOID79
CURRENT PELLING DATE: 2001-01-29
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US-09-770-689A-3
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US-09-770-689A-3
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Best Local Si
Matches 54;
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APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: C.001098
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                                                                                                                                                                           APPLICANT: Rosen et al.
TILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: 1721UN NUMBER: US/09/764,870
CURRENT APPLICATION NUMBER: 2001-01-17
Prior application data removed · consult PALM or file wrapper NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SFO ID NO 546
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Publication No. US20030077808A1
GENERAL INFORMATION:
TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
CURRENT APPLICATION NUBBER: US/09/764.891
CURRENT FILING DATE: 2001-01-17
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2e-16;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                               : Sequence 546, Application US/09764870
; Patent No. US20020042386Al
; GENERAL INFORMATION:
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: Publication No. US20030022229A1
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Best Local Similarity 100.0
Matches 52; Conservative
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US-09-764-891-5924
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US-09-764-870-546
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US-09-764-870-546/c
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100.0%; Pred. No. 2+-16;
Live 0; Mismatches 0; Indeis
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Title OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764.870
CURRENT APPLICATION DATE: 2001-01-17
PLIOT APPLICATION data removed - consult PALM or file wrappyr
NUMBER OF SEQ ID NOS: 646
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FILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodics-FILLE REFERENCE: PT214Cl
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Pair:
NUMBER OF SEQ ID NOS: 646
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CURRENT FILING DATE: 2002-04-19
PTION APPLICATION removed - See File Wrapper or Palm NUMBER OF SEQ 1D NOS: 646
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Sequence 546, Application US/10125540 ; Publication No. US20030059875Al ; GENERAL INFORMATION:
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: Patent No. US20020042386Al
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SEQ ID NO 546
LENGTH: 6461
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: ORGANISM: Homo sapiens
US-10-125-540-546
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US: 09-764-870-545
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Best Local Similarity
Matches 52; Conserv
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                                                                                                               SEQ ID NO 545
LENGTH: 5351
TYPE: DNA
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US-09-764-877-2678/c
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUTLE OF

TITLE OF INVENTION: ACID MOLECULES ENCOBING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THERE MOLECULES ENCOBING HUMAN KINASE PROTEINS, AND USES

FILE REFERENCE: CLOOLOGG

COURENT APPLICATION UNMBER: US/09/801,861

CURRENT FILING DATE: 2001-03-09
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Astibadies File REPERENCE: PCODE
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-7
PTIOT application data removed - consult PALM of 1.10 William SOFIWARE: PSC 10 NOS: 10231
SOFIWARE: Patentin Ver. 2.0
                                                                                                                            Score 52: DB 9: Length 5:32:
Pred. No. 2.3e-16:
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Live 0; Mismatches 0; Indeis
                                                                                                                                                                           0; Indels
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Best Local Similarity 100.0%; Pred. No. 7.1e-;6;
Matches 51; Conservative 0; Mismatches 5;
                                                                                                               FastSEQ for Windows Version 4.0
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Publication No. US20030077808A1
GENERAL INFORMATION:
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Patent No. USZ0020119544A1
GENERAL INFORMATION:
APPLICANT: YAM, Chunhua et al.
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Best Local Similarity 100.0
Matches 52; Conservative
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Best Local Similarity 100.0
Matches 52; Conservative
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US-09-764-891-6418
                                       /r TYPE: DNA
// ORGANISM: Homo sapiens
US-10-224-562-3
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US 09-764-891-6418/C
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US 09-801-861-3/c
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LENGTH: 17904
                  LENGIH: 53332
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SEQ ID NO 3
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SEQ ID NO 3
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                                                                                                                                                  Prior application data removed - refer to PALM or file wrapper NUMBER OF SEC ID NOS: 4031
SCFTWARE: Patentin Ver. 2.9
SEQ ID NO 2678
LENGTH: 26591
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APPLICANT: Horne, farri T.
APPLICANT: Wockley, Joseph G.
APPLICANT: Schert, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CORRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
                                                     GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC0005
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APPLICANT: L., Zoumen
APPLICANT: L., Zoumen
TITLE OF INVENTION: Inhibition of Histone Deaceylase
FILE REFERENCE: 106101,229
CURRENT APPLICATION NOMBER: US/09/563,728A
CURRENT FILING DATE: 2000-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 1.8%; Score 51; DB 10; I
Best Local Similarity 100.0%; Pred. No. 7.3e-16;
Matches 51; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7.9e-16;
Matches 51; Conservative 0; Mismatches 0;
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PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NGS: 36
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Sequence 2678, Application US/09764877 Patent No. US20020147140A1
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US-09-563-728A-36
US-09-563-728A-36
Sequence 36. Application US/09563728A
Publication No. US20030078216A1
GENERAL INFORMATION:
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ORGANISM: Homo sapieus
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US-09-764-877-2678
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RESULT 36

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3669 CACCTIGGCCICCCAAAGIGCTGGGATTACAGGCATGAGCCACTGGGCC 3718
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US-09-764-891-7810
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LENGTH: 11618
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LENGTH: 14216
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                                                                                         RESULT 41
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US-09-880-107-3814
                                                                                                                                                                                                                                                           Ouery Match 1.8%: Score 51; DB 10: Length 198285; Bost Local Similarity 100.0%; Pred. No. 8.1e-16; Matches 51; Conservative 0; Mismatches C; Indels C;
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HITLE DE INVENTION: Nucleic Acids, Proteins, and Antibodics-
FILE REPERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/744.869
CURRENT FILING DATE: 2001-01-17
PLIOR APPLICATION data removed - refer to PALM of 110 wildjest NUMBER OF SEQ ID NOS: 2442
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100.0%; Pred, No. 2.2e 15;
LVE 0; Mismatches 0; Todels
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IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE KERERERGE: PC007Cl
CURRENT APPLICATION NUMBER: US/10/C91,504
CURRENT FILING DATE: 2002-03-07
NUMBER OF SEQ 1D NOS: 2442
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SCFTWARE: Patentin Ver. 2.0
SEO ID NO 1779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1779, Application US/10091504 Fublication No. US20030059908A1 GENERAL INFORMATION:
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Fatent No. US20020061521A1
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100.0%; Pre-
PRIOR APPLICATION NUMBER: US 60, PRIOR FILLNG DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3814 LENGTH: 198285
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SEQ 1D NO 1779
LENGTH: 5819
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Matches 50; Conservative
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US-09-764-869-1779
                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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US-10-091-504-1779
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US-10-091-504-1779
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Prior application data removed - consult PALM or file wrapper
NUMBER OF SEC ID NES: 10241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ 1D NOS: 10231
SOFTWARE: Patentin Ver. 2.0
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                                                                                                             FILE REFERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: NOSCH et al.
ITLE OF INVENTION:
TILE PEFERNCE: PC006
CURRENT APPLICANTION NUMBER: US/09/764,891
CURRENT APPLICANTION NUMBER: US/09/764,891
                                                                    APPLICANT: Rosen et al. IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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hes 0; Indels
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TILLE OF INVENTION: NECHES ACIDS. Proteins, and Antibodies
FILE REFERENCE: Proof.
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7, 2,3e-15;
0;
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100.0%; Pred. No. 2.3
ative 0; Mismatches
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CORRENT FILLING DAIE. 2001 SL 17
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; Publication No. US20030077808A1
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: Sequence 9890, Application US/09764891
: Publication No. US20030077808A1
: GENERAL INFORMATION:
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Best Local Similarity 160.0
Matches 56; Conservative
                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.0
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US-09-764-891-7810
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US-09-764-891-9890
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Vert. 4.15

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Best Local Similarity 100.0
Matches 50; Conservative
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US-09-764-891-7809
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100.0%; Pred. No. 2.46 (5)
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOK
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Antibodies
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TITLE UF INVENTION: Nucleic Acids. Proteins, and Antibu FILE REFERENCE. PCOOR

FILE REPERENCE. PCOOR

CURRENT APPLICATION NUMBER: US/09/764,891

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult FALM of file w NUMBER OF SEQ ID NOS: 10231

SOFTWAKE: Patentin Ver. 2.0
                                                                                                                           1.7%; Score 50; 68 9; ix
100.0%; Pred. No. 2.4e-15;
Live 0; Mismatches 0;
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Matches 50; Conservative 0; Mismatches
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OTHER INFORMATION: n equals a,t,g, or c
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                                                                                                                                                                                                                                                                                                                                                                : Sequence 9966, Application US/09764891
: Publication No. US20030077808A1
: GENERAL INFORMATION:
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                                                                                                                                                 Best Local Similarity 100.0
Matches 50, Conservative
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US-09-764-891-8807
                                        , TYPE: CNA
: URGANISM: Homo sapiens
US-09-764-891-9967
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ORGANISM: Homo sapiens
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LOCATION: (4480)
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US-09-764-891-9966
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; SEQ 1D NO 9967
; 1.ENGTH: 19929
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Query Match

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                                           Gaps
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US-09-764-891-9446
Sequence 9446. Application US/09764891
Squence 9446. Application No. US20036077808A1
GENERAL INFORMATION:
SAPLICATION NO. US20036077808A1
STILE OF INVENTION:
TILLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT APPLICATION NUMBER: US/09/764,891
STILE REPERENCE: PCOOR
SUBPLICATION NUMBER: US/09/764,891
SOFTWARE PAPEL ALL REPORT OF THE STILE WINDER OF SEQ ID NOS: 10231
SOFTWARE PAFENTIN VET. 2.0
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                                                                                      1187 CIGCCCACCITGGCCICCCAAAGIGGGAITACAGGCAIGAGCCACIG 1236
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                                                                                                                 4160 CTGCCCACCTTGCCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACG 4113
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: 00006
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed · consult PALM or file wrapper
NUMBER OF SEQ ID NUS: 10241
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                                        Indels
             Pred. No. 2.4e-15;
Mismatches 0;
100.0%; Pred. ...
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1.7%; Score 50; DB Best Local Similarity 100.0%; Pred. No. 2.4
Matches 50; Conservative 0; Mismatches
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APPLICANT: Jonsdottir, Sit
APPLICANT: Heynisdottir, Signidur Th.
TITLE OF INVENTION: HIMAN STROKE GENE
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: Publication No. US2U030054531A1
: GENERAL INFORMATION:
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US-09-764-891-9446
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US-09-764-891-7809
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Sequence 2616, Application US/09918995
Sequence 2616, Application US/09918995
GENERAL INFORMATION:
APPLICATION NO. US2003007362341
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEGUENCES OBTAINED:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEGUENCES OBTAINED:
TITLE OF INVENTION: NOVEL US/09/938,995
CURRENT APPLICATION NUMBER: US/09/238,076
PRIOR APPLICATION NUMBER: US/09/238,076
PRIOR FILLING DATE: 2001-07-30
PRIOR FILLING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOUTHWARE: FESSED FOR WINDOWS VEISION 3.0
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TITLE OF INVENTION: 29 Human Secreted Fro; eins
TITLE OF INVENTION: 29 Human Secreted Fro; eins
TITLE OF INVENTION: 29 Human Secreted Fro; eins
TITLE OF INVENTION: 201591
CURRENT APPLICATION NUMBER: 08/09/729,855
CURRENT FILING DATE: 2000-12-06
PRIOR APPLICATION NUMBER: 09/055,270
PRIOR APPLICATION NUMBER: 60/056,270
PRIOR APPLICATION NUMBER: 60/056,271
PRIOR APPLICATION NUMBER: 60/056,271
                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ 1D NO 1
                     CURRENT APPLICATION NUMBER: US/10/067.514 CURRENT FILING DATE: 2002-02-04 PHIOR APPLICATION NUMBER: US 09/811/352 PRIOR FILING DATE: 2001-03-19
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. Sequence 11, Application US/09729835

: Patent No. US20010016647A1

: GENERAL INFORMATION:
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; OTHER INFURMATION: n = A,T,C or G
US 09 918 995 2616
FILE REFERENCE: 2345.2010-003
                                                                                                                                                                                                                                                                                                                             Usery Match
Rest Local Similarity 100.0
Matches 50: Conservative
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                                                                                                                           NUMBER OF SEQ ID NOS: 84
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                               TYPE: UNA
ORGANISM: Human
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LENGTH: 448
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Matches
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Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 49; Conservative 0; Mismatches 0; Indels
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Job time : 3143.36 secs
PRIOR FILING DATE: 1997-08-29
PRIOR APPLICATION NUMBER: 66/056,073
PRIOR FILING DATE: 1997-08-29
NUMBER OF SEO 1D NOS: 128
SOFTWARE: Patentin Vel. 2.0
                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
LOCATION: (37)
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                                                                                                                 SEQ ID NO 11
LENGTH: 866
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AAV57926 AAV57903 ABN65629 AAI64613	AAS31466 ABQ66790	ABQ66791 AAK65197 AAL03236	ABA18026 ABA20511 AAK70791 AAK78512	AAC25949 ABV03782	ABV12951 ABV13744	4BV04575	ABV34857	4BV42939	QA18/908 QBV43803 QBV04619	ABV02959	4BV33273	ABV43707 BRV32646	ABV41571	ABV42196 ABV43750	ABV21487	ABV21910 ABV22485	ABV22952	ABV27742	ABV28300 ABV28752	ABV28784	ABV12128 ABV11501	ABV02332	ABV13788 AAK77921	AA164545	ABA07913	AAL03730 AAL36313	AAS34422	AAC89560	AA286967 Abkra4699	ABN97319	AA191676 AAT26600	AAF67515	ABV57113 AAH92172	ABK47950	AAH51743 AAC36279	ABA21246	AAL07202	AAK87088 AAS33447	AAL05122 ABL98014
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β		CTATGAATCCTTCAGGGCAGATTCATATTAGACTCTTCACAGTTTGACCTGAGTTT	1800
qo	1741	CTTCIATGALCCTTCAGGGCAGATCATAITTAGACTCTTCACAGTTTGACTGTGAGTTT	1800
ςλ		TOUCCAGAALAAGGIGACATTTAGTTTGTTGGCTTGATGGATGACTTAAATATTTAGACA	1860
qq		GGCCAGAATAAGGT GACATTTAGTTGGCTTGATGGATGACTTAAATATTTAGACA	1860
à á	1861	T0GTGTGTGTAGGCTGGATTGCTACTCTTGCCTTTTTTTTTGCCCCTCCAGTGTTTTGGGT	1920
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S q	1921	ACTITION CONTROLL AND CONTRACTOR AND CONTROLL OF THE CONTRACTOR AND CONTRACTOR AN	1980
Oy	1981	TIACACGACTGCAATTCTCTGGCTGCACTTCACAAATGTATACAAACTAAATACAA	2040
qu	1981	AATTCTCTGGCTGCACTTCACAAATGTATACAAAATACAA AATTCTCTGGCTGCACTTCACAAATGTATACAAAAAAAAA	2040
Oy	2041	NICACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	2100
Op	2041	CCTGTGT TTTTATCACAGGGAGGCTGATCAATATAATGAAATTAAAAGGGGGCTGGTC	2100
ςò	2101	IATTGITCTCTCTGTTTTGTTTGTTTTGTTTGTTTCTTTTTTTT	2160
Op	2101	ATATIGITETETETTTTTTTTTTTTTTTTTTTTTTTTTTT	2150
QY	2161	ICTCAA TITATGAAGAGAAGCAGTAAGATGTTCCTCTCGGGTCCTCTGAGGGA	2220
QQ	2161	CCTTCCTCTCAATTTATGAAGAGAGAATAAAAATGTTCCTCTCGGGTCCTCTGAGGG	2220
Oy	2221	TGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTC	2280
qq - ·	2221	CTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTAGGTCGCCTATCAAAATCAAAGTC	2280
Qy	2281	TGTGGGGGGAAAAAGCAGCCCATTACCCAGAGGACTGTCCGCTTCCCCT	2340
QQ	2281	AGGITTGIGGGGGAAAAAAAAAAGCAGCCCAITACCCAGAGGACTGICGCCTTCCCCT	2340
97	2341	AUCTIAGOCTTIGAAAGGAAACAAAAGACAAGACAAAATGATICGCGICCTGA	2400
Db	2341	ACCCAUCTIAGUNCT TTGAAAGGAACAAAAGAAAGAAGAAAATGATTGGCGTCCTGA	2400
άγ	2401	CCCCCCAATCCCTCCCTCCGGCTGAGGAACTAAC	2460
Ob	2401	SGAGATTCAGGCTAAGAGTCTCTCTCCCCCAATCCCTCCGGCTGAGGAAACTAAC	2460
Ś	2461	AAAAAAAA TCCCGGAAAGCAGCATTFAGAGGAAGCAAATTCCACTGGTGCCCTT	2520
qq	2461	AAGCAGGATTTAGAGGAAGCAAATTCCACTGGTGCCCTT	2520
ςλ	2521	GAGAGTCTGCGCGCAGCCCGAGCCCAGCGCTTCCCGC	2580
ব্র	2521	3CTGCCGGGAACGTGGACTAGAGAGTCTGCGGGGGGGGCGCGGAGCCCAGGGGTTCCCGC	2580
ογ	2581	SICITAGGCCGGCGCGGGGGGGAAGGGGAACGCAGACCGCGGAACCCTAAGACA	2640
qa	2581	GCGTCTTAGCCCGCGCGCGCGGGGGGGGGGGGGGGGGGG	2640
Qy	2641	SCACCCACCCACCACCTCCCCCCAACTCCCTAGATGTG	
qq	2641	TGCTGTACCCTCCACCCCACCCCACCCACCCCCCCCCAACTCCCCTAGATGTG	2700
ς	2701	TCCTGGCCGGCTGACGTCGCCCGTTTAAGGGGCGGGCCCGGGTCCACGTGCTTCTGC	2760
qu	2701	TGGCCCCCCCCCCCCCTTTAAGGGCCCCCCCCCCCCCCC	2760

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                                                                                                                                                                                                                                                              isolated nucleic acid useful for modifying the ATP-Crudina cassette lacked) and screening for candidate modulatory compounds or substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTELLIFELLELLELLELLELLELLE ELLE ELLE TELLE TELLE TELLE ELLE E
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GACTOCAGAATTCOTTGCCTGGTGGCCTCCACATGCACGGGGGGCTGCTTGGGGGTCTC FFEFFFFFFFFFFFFFFFFFFFFFFFFFFCGAGAGGCTGCAGGGCTTGCAGGGCTTGCAGGGCTCCACATGCAGGGCTTGCAGGGCTCCACATGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCTTGCAGGGCCTTGCAGGGCCCTTGCAGGGCCTTGCAGGGCCCTTGGCAGGGCCTTGCAGGGCCTTGCAGGGCCTTGCAGGGCCCTTGGCAGGGCCTTGCAGGGC
TICTATGGGTCTGTCCTGAGTGTTGATAGAACGACTGATGTGAGTACGTGGGGTTGAGCGTTGAGCGTTGAGCGTTGAGCGTGTTGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGCATGATGAGAGAGCATGATGAGAGAGCATGATGAGAGAGA
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TGCAGCTGGTGCAGTTCTGGANTATGATGGAGCTGGAGGTGGSAAGAGAGAGTTG 
GGCCAGCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTTT 
AAATGTGAATCTGCCCTTCAAGGTGCCTACAAAGGTATTTTTTTT
GTGBCCTCACGTGCACTTCCAGGGCCTGGGCTCTTCTTCTACAGGTCTGGTGGTGGTGGTGGTGTGTTTTTTTT
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GECCIGEOTITITATCACAGGGGGGGGTCATCAATAAAGAAATAAAAGGGGGGTGGTC 
CATATTGTTCTGTGTTTTTGTTTGTTTGTTTTTTTTTTT
TCCTTCCTCTCAATTAATGAAGAAGCAGTAAGATGTTCCTCTCGGGTCCTTTGAGGGATTTTTTTT
CCTGGGGAGCTCAGGCTGGGAATCTCCAAGGCAGTTGGCTATCAAAATCAAAGTC FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
CAGGITIGEGGGGGAAAAAAAAAGAGCCATTACCCAAAAGACTGFCGGCTTOCCT

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                               341 CACCCCAGCCTAGGCCTTTGAAAGGAAACAAAAGACAAGACAAATGATTGGCGTCCTGA
                                                                                              401 GGGAGATTCAGCCTAGAGCTCTCTCCCCCCAATCCCTCCGGCTGAGGAAACTAAC
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XENO-) XENON GENETICS INC.
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23-JUN-2000; 2000US-0213958.
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          freating a lower than normal high density lipoprotein-cholesterol (HBL-7) level, a higher than normal trigiveride level, or a cardiovascular disease, by administering a compount that medulates LXR-or EXXE-mediated transcriptional activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             962 TATTITICITGACACGGAGICITIGCICIGICACICAGAGIGAGIGAGIGATATAT ICZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1202 TCCCAAAGIGCTGGGATTACAGGCATGAGCGGTATGCGGCTTAGATGTATTG [261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        902 CIGGGCCITGGGCITIAGAAAGCICAIGTCTGGCCITTGIGAGAI CAICCITTT 941
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                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 183999 BP: 49549 A: 37944 C: 41170 G: 54950 T: 486 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for treating a justical diagnosed as having a lower than formal higo-density lipoprotein-cholesterol (HDL-C) level, a nighter than moral triglyceride level, or a cardiovascular disease, involving administering a compound that modulutes LXR- or XXX-mediated transcriptional activity or ABC1 expression or activity. The LXR gene product may be used in an assay to intentity compounds useful for the treatment of a disease of condition selectinglyceride level, and a cardiovascular disease.
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                                                                          Claim 8; Fig 1; 317pp; English
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                             964;
                                                                                                                                                                                                                                                                      pery Match
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The present sequence represents the 5' flanking region of the huuman adenosine tripkusphate (ATP) binding cassette protein (AbC) 1 gene. ABC1 resides in cell membranes and utilises ATP hydrolysis to transport a wide variety of substrates across the plasma membrane. ABC1 is a privotal protein in the apolipoprotein-mediated mobilisation of intracellular cholesterol stores. ABC1 is defective in Tangler disease, a genetic disorder characterised by abnormal HDL-cholesterol metabolism. The ABC1 gene is localised to chromosome 9422-9431. The ABC1 genes and proteins are useful for developing pharmaceutical agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and atherosclerosis. The quenes are useful for developing screening assays to screen for compounds that regulate the expression of genes associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adenosine triphosphate (ATP) binding cassette (ABC) polynucleotide, useful for the development of agents for the treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                    Nucleotide sequence of the 5' flanking region of the human ABCl gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; adenosine triphosphate binding cassette protein 1; ABC1; apoliopprotein mediated mobilisation; cholesterol; Tangier disease; chromosome 9422-943; heart disease; hypercholesterolemia; atherosclerosis; cholesterol transport; ss.
                                                                                       GCAGGTGG13GGAGTTCTGGAATATGATGAAGCTGGAGGTGGGAAGAAGAGAGTAGGCTTGG
                 GGCAGCTCTCTCTCATGCCACCTCATTCTGGCCAAAACTCAGGTCAAACTGTGAAGAGTCTA
                                                                                                                                                                             27511 AATGTGAATCTGGCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGGCCTTG
                                                                                                                                            AATGTGAATCTGCCCTTCAAGGTGGCTACAAAGGTATCTTTGTCAAGGTAGGAGCCTTG
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990S-0153872,
990S-0166573,
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14-SEP-1999;
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                                                                                                                                                                                                                                                                                       2310 CCATTACCCAGAGGACTGTCCGCTTCCCCTCAGCCTAGGCCTTTGAAAGGAAAC 2469
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20
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                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; ademosine triphosphate binding cussette projein [: Ab[]]; applipportotein mediated mobilisation; cholesterol; langue; cisease; eficomosome 9q22-9q31; heart disease; hypercholesterolungua; atherosclerosis; cholesterol transport; ss.
with cholesterol transport. The genes and proteins are also useful are also useful as diagnostic indicators of cardiovascular disease other disorders associated with hypercholesterolemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2130 TITGITIGITICITITITIGITITIGEGOCCICCITCCTCCAATTAATGAAGAAGCA
                                                                                                                                             TTTAGAGGAAGGAAATTCCACTGGTGCCCTTGGCTGCCGGGAAGGTGGAGGTGGAGTGT
                                                                                                                                                                                                                                                                                                                                           AAAAGACAAGACAAAATGATTGGGGTGCTGAGGGAGATTCAGCCTAAGACTGTTTTTCAC
                                                                                                                                                                                                                                      Nucleotide sequence of the 5' flanking region of the burnar ASCI
                                                                                                        Indeis
                                                     Sequence 1643 BP; 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                            Score 541; DB 22; L
Pred. No. 1.7e-236;
                                                                                                         0
                                                                                                        Mismatches
                                                                    18.7%; Score
100.0%; Pre-
0; h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF24704 standard; DNA; 1643
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                                                                                                      Matches 541; Conservative
                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                     Adenosine triphosphate (ATP) binding cassette protein (ABC) 1 polynucleotides and polypeptides, useful for treatment of heart disease and other disorders associated with hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.7%; Score 541; DB 22; Length 1643; 100.0%; Pred. No. 1.7e-236;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1643 BP: 370 A; 413 C; 457 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders associated with hypercholesterolemia.
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                                                                                                                                                                                                                                                            Garvin
                                                          990S-0153872
990S-0166573
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                                                                                                                                                           (CVTH-) CV THERAPEUTICS INC
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Matches 541; Conservative
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                        18-JUN-1999;
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19-NOV-1999;
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The invention relates to an isolated human large AJF binding cassette transporter 1 (ABC1) promoter capable of directing transcription of transporter 1 (aBC1) promoter capable of directing transcription of heterologous coding sequence positioned downstrear in it. in. ABPT promoter is useful for expressing foreign bind in a hest of 1. by introducing into the host cell a gene transfer vertus ceptising the promoter operably linked to a foreign bNA is expressed. The selectionary polymetride or RNA, where the foreign DNA is expressed. The selectional the gene introduced into the host cell by adenovirus interior. The selection or transfer, topical application to the cell or microhogetion. The gene transfer comparison and expresses a reporter molecule. The method further involves introducing into the cell a gene transfer vector comparison a nucleic acid segment encoding a transactivator protein capable of upregulating the ABC1 promoter, or contacting the cell with the transactivator protein, or an agonist of the transactivator protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding cassette transporter 1(hABG1) promoter sequence.
                                    capable of directing transcription of Leterologous coding sequence positioned downstream to it, useful for expressing foreign fixe in host cells ^{\circ}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, large ATP-binding cassette transporter 1, ARCI, promoter; antiarteriosclerotic, gene transfer, transactivator, ds.
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Pred. No. 2.7e-181;
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99.8%;
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ABL58400
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bacterial infection; fungal infection; autoimmune disorder; burn; rheumatoid arthritis: multiple sclerosis; autoimmune thyroiditis; diabetes; allegy; asthma; neurodegenerative disease; Crohr; s disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; timour; coaquiation disorder; haemophilia; inflammatory disorder; ricer; tissue regeneration; wound healing; haematopolesis; myeloid deficiency;
                                                                                                                                                                                                             2369
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                                                                                                                                                                                                          2310 CCATTACCCAGAGGACTGTCCCCTTCCCCTCACCCCAGCCTAGGCCTTTGAAAGGAAAC
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ss; gene: secreted protein; immune deficiency; viral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA for novel secreted protein, SEQ ID 344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK34575 standard; cDNA; 2890 BP.
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ABK34575/C
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Six hundled and twenty five polynucleotides derived from a variety of

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/standard_name- "Single nucleotide polymorphism, SNP" 4464..570]
/*tag- n
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/*tag= k
/standard_name= "Single nucleotide polymorphism, SNP"
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/standard_name- "Single nucleotide polymorphism, SNP"
replace (5982,A)
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/stadard_name= "Single nucleotide polymorphism, SNP"
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replace (3983,A)
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                                                                                                             "RLBP1"
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replace (7704,T)
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                                                                                                                                                                                    (4061,C)
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   a variety of human tissue sources and which encode covel secreted proteins, their complements and sequences that hybridise to them.

Also included are a vector comprising the polynomical decreted proteins and included are a vector comprising the polynomical decreted by the polynomical proteins and identification of modulators of the proteins of the proteins and identification of modulators of the proteins of the protein conditions and proteins the the treatment of various immune deficienties and disorders (e.g. rheumatoid arthritis, muitiple selections, autoimmune disorders (e.g. rheumatoid arthritis, muitiple selections, cautoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, parkinson's disease, liver fibrosis, coaqulation disorders (e.g. haemophilia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         =;
                                                                                                          The invention relates to 625 polynucleotides which have been derived from
                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopolesis, for treating myeloid or lymphoid cell deficiencies. The present sequence is one of the 625 cDNA sequences
human tissue sources which encode secreted proteins, useful for
treating immune deficiencies and disorders such as autoismuse disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace (3647,A)
/*tag= d
/standard_name- "Single nucleotide polymorphism, SNP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1187 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGGCACTGTGGCTT241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1666 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCATTGGGCCC 2612
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8.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ry Match 1.9%; Score 55; DB t Local Similarity 100.0%; Pred. No. 8.3 ches 55; Conservative 0; Mismatches
                                                                      Claim 1; Page 170-171; 339pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/*tag= b
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/*tag= e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding a secreted protein.
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The invention relates to an isolated polynoclopide, which comprises
genes and haplotypes of the retinal dehyde thinding protein [REBF] gene.
The polynucleotide comprises polymorphic sites in the RibPl gene, which
are referred to as PSI-24 to designate the order in which they are
located in the gene. Also included are methods for predicting a
genotyping the RibPl gene of an individual, a method for predicting a
leaplotype pair for the RibPl gene of an individual, a method for predicting a
leaplotype pair for the RibPl gene of an individual, a method for propertion of the RibPl gene of an individual, a method for design of a least one
dentifying an association between a trait and at least one caplotype or
haplotype pair of the RibPl gene, a composition comprising a new recomposition comprising a set of oliquincieotides designed to denotype each
of PSI-PS24 recompliant non-human organism transformed to enocype each
of PSI-PS24 recompliant non-human organisms transformed to enocype each
of PSI-PS24 recompliant non-human organisms transformed to enocype or transfected
with the isolated polymorphic variant sequence or expresses an RibPl
protein encoded by the first nucleotide sequence or expresses an RibPl
protein encoded by the polymorphic variant sequence or a proprietion
of a reference sequence for the RiBPl protein or its fragment,
an anti-RiBPl antibody, a method for screening to aruqs taracting the
solated polypeptide, and a computer system for storing and adapting the
protein encoded protein and a computer system for storing and adapting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genetic variants having polymorphisms in the retinaldelyde-binding protein 1 gene, useful for studying the function of and for expressing RLBP1 protein for use in screening drugs for treating diseases related to RLBP1 activity.
                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "Single nucleotide polymorphism, SNP"
12576..12734
/*tag= ak
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/standard_name= "Single nucleotide polymorphism, SNP"
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                                                                                         "Single nuclectide polymorphism, SNP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Fig 1: 107pp: English.
                                                     replace (11384,A)
                                                                                                             replace (11386,A)
                                                                                                                                                                   replace (11411.C)
                                                                                                                                                                                                                                                                                                                                         replace (12531,C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       replace (12587,1)
replace (11343,G)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gene for retinaldehyde-binding protein 1, RLBP1, geneiic sequence.
expressing RLBPI protein for use in screening candidate drugs to treat diseases related to RLBPI activity (e.g autosomal recessive retinitis pigmentosa (arRP). The methods and haplotypes are useful in improving the efficiency and output of several steps in the drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. These are also useful for designing clinical trials of candidate drugs for treating a specific condition or disease, as well as for screening compounds targeting RLBPI to treat a specific condition or disease predicted to be associated with RLBPI activity. The kit and method are useful for determining whether an individual has one of the haplotypes
                                                                                                                                                                                                                                           or haplotype pairs cited above. The transgenic animals are useful for studying expression of the RLBPl isogenes in vivo, for in vivo screening and testing of drugs targeted against RLBPl protein, and for testing the efficacy of therapeutic agents and compounds for retinal diseases in a biological system. The gene for RLBPl is located on chromosome 15q26. The present sequence is the gene for RLBPl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD 10046 CCCACCTTGCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAG: 9992
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 13645;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9%; Score 55; DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No.
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Matches 55; Conserv
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polypeptide comprising an amino acid sequence that is a polymorphic variant of a reference sequence for the RiBPI protein of the reference sequence for the RiBPI protein of its fragment.

Solated polypeptide, and a computer system for true and analysing to polymorphism data for the RIBPI oncogene gene.

The polymorbhism data for the RIBPI oncogene gene to storing and analysing polymorphisms in the RIBPI, and in the polymorphism data for the RIBPI oncogene gene to storing and analysing polymorphisms in the RIBPI, and in the object of RIBPI oncogene gene of storing and analysing the expression and function of RIBPI, and in expressing RIBPI protein for use in screening candidate drugs to treat diseases related to RIBPI activity (e.g. autosomal recessive retinitis pigmentosa (arRP). The methods and haplotypes are useful in improving the efficiency and output of several steps in the drug discovery and development process, incidinging ariget, validation, dennitying lead compounds, and early phase clinical trials. These are treating a specific condition or disease compounds targeting RIBPI to treat a specific condition or disease compounds targeting RIBPI to treat a specific condition or disease.
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haplotype pair for the RLBP1 gene of an individual, a method for identifying an association between a trait and at least one haplotype or haplotype pair of the RLBP1 gene, a composition comprision at least one genotyping oligonucleotide for detecting a comprishism it the RLBP1 gene at a PS consisting of PSI-PS24, a kit for genotyping the RLBP1 gene of an individual comprising a set of oligonucleotides designed to genotype each of PSI-PS24 recombinant non-human organisms transformed or transferred with the isolated polynucleotide, where the organism expresses a RLBP1 protein encoded by the first nucleotide sequence or expresses an KLBP1 protein encoded by the polymorphic variant sequence or expresses an RLBP1 protein encoded by the polymorphic variant sequence an isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases in a biological system. The gene for RLBP) is ideated on chromosome 15926. The present sequence is a representation of the gene for RLBPI encompassing all the single nucleatide polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for determining whether an individual has one of the hapicrypes or haplotype pairs cited above. The transpenic animals are useful for studying expression of the RLBPI isouenes in vivo, tor in vivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening and testing of drugs targeted against RLRS1 protein, and ror
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960S-6724394.
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les 55; Conservative
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unaffected by hereditary harmonomous (HH). Also described is a method to determine the presence or absence of the common hereditary harmonomous (HH). Also described is a method to determine the presence or absence of the common hereditary harmonomous (HF) game mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (HT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a Roket gene and antagonists of BT function. Also described are: (1) a Roket gene which can be used to develop products for the study, diagnosis and treatment of lupus and Slogren's syndrome, and (2) NPT3 and can can homologues of a type I sodium transport gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine butyrophilin: BT: human hereditary haemochromatosis: HFE: diaquosis: iron metubolism: NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF5; milk protein: lupus: Sjogren's syndrome; hypophosphatemia; type I sodium transport gene: Ss.
                                                                                                                                                                                                                                                                                                      products from the human haemochromatosis gene. The present equence represents a hereditary haemochromatosis subregion from an individual
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                                                                                                                                                          Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
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                                                                                                                                                                                                                                                                                  The present invention describes hereditary haemochromatosis gene
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                                                       Ruddy DA, Thomas WJ;
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Pred. No. 8.3e-15;
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                                                       Lauer PM,
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                                                                           Suchihashi Z, Woltt RK;
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                 (PROG-) PROGENTIOR INC.
                                                     Kronmal GS.
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                                        Hereditary haemochromatosis gene products—used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                            Human; cytostatic; gene expression; gene mapping; tiss or profilent:
                                                                                                                                                                                                                                                             Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70509 T; 0 other;
                                                                                                                                                                                                                                                                              Length 237326;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garcia PD, Sudduth-Klinger J. Reinlard C. Scott EM, Zhang G, Kussam A, Fot D, Jabal
Thomas W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                         Human cancer related polynucleotide SEQ ID Ni 55 m
                                                                                                                                                                                                                                                                             1.9%; Score 55; DB 19; I
100.0%; Pred. No. 8.3e-15;
Ruddy DA,
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                                                                                                                                                                                                                                             similarly be used for hypophosphatemia.
Lauer PM,
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                                                                         Claim 1: Fig 9: 209pp; English.
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       Tsuchihashi 2, Wolff RK;
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Kronmal GS,
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                       WPI; 1998-240014/21.
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Matches 55; Conserv
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                                                         metabolism
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                                                                                                                    with cytostatic activity. The polynucleotide is used to produce a polypeptide, to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and to inhibit tumour growth. The polynucleotide is used as morph in mapping and tissue protiling. The encoded polypeptide and antibodies to the polypeptide can also be used for therapoutic and diagnostic purposes. The polynucleotide is useful for
                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                       invention relates to an isolated polynucleotide (ABN27253-ABN33262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human riboscoral Sli protein 12 and encoded polynucleotide, applicable in diagnosis and treatment of malignant tumour, haemopathy, human immunodeticiency virus infection, immunological discases and
New nucleic acid for producing a polypeptide, detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, and inhibiting tumor growth -
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
human immunodeficiency virus: HIV; infection; immunological disease;
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                                                                    Claim 1; SEO ID NO 5596; 883pp + Sequence Listing; English
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/note- "claimed in claim 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human ribosomal S11 protein 12 encoding cDNA
                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
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Claim 5, Page 29 for App. Chinese

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  Human, secreted extracellular matrix protein; ds; immunicodulatory; Anti-HIV; antianemic; antirheumatic; antisclerotic; cardian; vascular everbroprotective; thrombolytic; antimicrobial; ophthalm:: cytostatic; antialzheimers; immune/autoimerseses; HIV infection; asaemia; human immunodeficiency virus; rheamatoid arthitis; muisiple solerosis; cancers; hyperproliferative disorder; breast neopiasm; relancema
                  cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic activity. The proletin and encoding polymeticolide are used in diagnosis and treatment of malignant tunnour, haemopa'hy, branan immunodeficiency virus (HV) infectious, immunoicotica, diseases and various inflammations. The polymucleotide is useful in seme therapy.
                                                                                                                               Gaps
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Alzheimer's disease; Parkinson's disease; cardiovascular diserder;
cardiac arrest; tachycardia; angina; infection; corneal infections:
                                                                                                                                                                                                                                                                                             Human DNA for a novel extracellular matrix protein, Seq 10 No 545.
            The invention relates to the human ribosomal S11 protein 12 with
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                                                                                                                                                               Score 52, DB 22, Length 1374;
Pred, No. 2e-13;
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                                                                                   Sequence 1316 BP; 338 A; 306 C; 297 G; 375 T; 0 ottor;
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Best Local Similarity 100.0%;
Matches 52; Conservative 0
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The invention relates to isolated mucleic acts as eaches ecoding nevel human secreted extracellular matrix proteins (SES). The polymediechdes and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, acats, hesses, cats, doas, chickens or sheep. For example, disolders associated with nerroased expression of SPS. The SP polymediectide or a vector expression them may be administered to treat diseases by gene thatapy. Antisense molernles may be administered to treat diseases by gene thatapy. Antisense molernles may be administered to down regulate expression of Sts by tending with the cells own genes and preventing their expression. The polymicieotides may also be used as DNA probes in diamostic assays. The SES may also be used as antigens to produce antibodies and to identity modulators. (agonists and antagonists) of the SES. The untilebales and antagonists may also be used to down regulate expression and activity of SE and as diagnostic agents for detecting the presence of SES in samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecules encoding human secreted extracelly, at matrix proteins, used in preventing, treating or amelforaling a discider, e. Alzheimer's and Parkinson's diseases and cancers
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include wound healing, maintenance of organs before transplantation, support of cell culture of primary tissues, modulation of for example
                                                               Gaps
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                                                                                    1193 ACCITGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC 1244
                                                                                                1.8%: Score 52; DB 22; Length 5351; 106.0%; Pred. No. 1.9e-13; Live 0; Mismatches 0; Indels (
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                                                 Best Local Similarity 100.0
Matches 52, Conservative
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 A NAMES O NAME
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Acti-HIV, actianemic, antirheumatico antisclerotico cardiano vascularo
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Note: The sequence data for this patent did not from part of the
printed specification, but was obtained in electronic formal directly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding human proteins, useful for diagnosis,
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cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immune/autoimmune disease; HTV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliterative disorder; breast neoplasm; metanoma; Sezary syndrome; Gaucher's disease; neurological diseases; Alzheimer's disease; cardiovascular disorder: cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
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The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPs). The novel human secreted extracellular matrix proteins (SPs). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs. chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as antigens to produce antibodies and to identify modifiators (agonists and actagonists) of the SPs. The anti-(SP) antibodies and antigonists and actagonists of the SPs. The anti-(SP) antibodies and catagonists and as diagnostic agents for down regulate expression and activity of SP and as diagnostic agents for detecting the presence of SPs in samples. The disorders include for example: immune/autoimmune diseases (e.g. HIV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (human immunodericiency virus) infections, anaemia, Theumatoid arthritis and multiple selerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (e.g. Alzheimer's disease), peurological diseases (e.g. Alzheimer's disease, Parkinson's disease), cardiocal cardio-cerebrovascular disorders (e.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungl and ocular disorders (e.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary tissues, modulation of for example
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                                                                                                                                                                                                                                                                                                                                          Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
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100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 546; 577pp; English.
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                                                                                                                                                                                                                                              Rosen CA, Barash SC, Ruben SM
08-DEC-2000, 200CUS-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251969.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0251990.
05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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Home sapiens

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(ABP47846-ABP48110) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agohists are useful. The diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's colitis; (c) cardiovascular disorders such as mycocardial ischaemias; (d) yound healing; (e) neurological diseases e.g. cerebral anoxia and parastic infectious. The present sequence is that of a
                                                                                                                                                                                                                                                                                                                                                                                                                                      polybuclectide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPIO at sequence.html?DocID-999909764870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antiges; cancer; cytostalic; gene therapy; vaccine; metastasis; ds.
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Watches 52; Conservative
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AAK65197
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         The invention relates to novel genes (ABO66521-ABG66785) and proteins
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05-JAN-2001;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Disclosure; SEQ 1D NG 20009; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
supplement the patients own production of (I). Additionally, (I)
to polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent.
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54920 and AAM82169
tepresent sequences used in the exemplification of the present invention.

Sequence 8319 BP; 2521 A; 1610 C; 1560 G; 2628 T; 0 other;

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2000US-0241809
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                            Length 8319
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                            1.8%; Score 52; DB 22; Le
100.0%; Pred. No. 1.9e-13;
Live 0; Mismatches 0;
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2000US - 0218290 .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides the protein and coding sequences of a number of human reproductive system related antiques. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a reproductive system antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 5924; 1297pp · Sequence Listing: English.
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             2000US 024924
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The invention relates to movel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast, and other cancers of the adrenal gland, bone marrow, breast, gastrontestinal tract, liver, lung, or urogenital: (b) immune disorders e.g. Addison's disease, altergies, autoimmune charmony tissues and pland, bone marrow, and utoin mune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis: (c) cardiovascular disorders such as mycocardial ischaemias: (d) wound healing: (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at 1tp.wipo.int/pub/published_pct_sequences.
Nucleic acids encoding 3224 human nervous system antigen polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                 useful for preventing, diagnosing and/or treating nervous system
                                                                       Disclosure; SEQ ID NO 10357; 1701pp + Sequence Listing; English.
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(HUMA-) HUMAN GENOME SCI INC

Raben SM Barash SC, Rosen CA,

WPI; 2001-541565/66.

Nucleic acids enroding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.

Disclosure; SEQ in No 12842; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and overian caccer and other cancers of the adrenal gland, bone, bone marrow, breast, qustrointestinal tract, liver, lung, or urogenital:

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2000US-022630
2000US-0236370
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13 - 0CT - 2000;
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20-0CT-2
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(b) Immune disorders e.g. Addison's disease, alleraies, autcimmune haemolytic anaemia, autoimmune thyroiditis, diabetes meilitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. retental anoxia and epilepsy; and (f) infectious diseases such as vira; barterial, fungal and parasitic infections.
                                                                                                                                                                           Note: The sequence data for this patent did not form past of the printed specification, but was obtained in electronic sural directly from WIPO at ftp.wipo.int/pub/published_pct.sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoletic; immune/haematopole'ic an'iqen; cancer:
cytostalic; qene therapy; vaccine; metastusis; ds
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UP 22210 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGGCGAATGGT, 22159
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100.0%; Pred. No. 1.9e-13;
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Matches 52; Conservative 0; Mismatches
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2000US -0220963
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2000US-0198123.
2000US-0205515.
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2000US-0214886.
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2000US-0216880.
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2000US-0225266.
2000US-0225267.
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2000US-0184664.
2000US-0186350.
2000US-0189874.
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20000S-0225759.
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                               Human immune/baematopoletic antiqen genomic sequence SEQ ID NO:33324.
                                                                    AAK78512 standard; DNA; 29329
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20000S-0224518.
20000S-0224519.
20000S-0225213.
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2000US-0216647
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22 - MAR - 2000;

17 - MAR - 2000;

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07 - JUL - 2000

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01-SEP-2000;
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                                   RESULT 23
AAK78512/C
                                                                                        AANSYST TO ARREATOR ENTOUGE THE HUMBOL INDEADY CONTRACTOR ALLEGE (1)
ACTIVITY, and can be used in gene therapy and varying cytestatic
activity, and can be used in gene therapy and varying contribution. (1)
proteins and polynucleotides may be used in the provention disancess and
treatment of diseases associated with inappropriate (1) expression. (2)
example, they may be used to freat disorders associated with decreased
example, they may be used to freat disorders associated with decreased
cytession by rectifying mutations of deletions in a parient's action
that affect the activity of (1) by expression inactive proteins or to
supplement the patients own produce the secreted (1), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein (1) proteins and polynuclectides may be assed or greaters and cancer metastases of haematopoictic derived rells. AAK6473
to AAK8764 represent human immune/haematopoictic during approprie
sequences from the present invention. AAK5442 to AAK545C and AAK82169
represent sequences used in the examplification of the present invention.
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                               2000US-0249208.
2000US-0249209.
2000US-0249210.
                                                                                 2000US-0249211.
2000US-0249212.
2000US-0249212.
2000US-0249213.
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2000US-0250160.
2000US-0250391.
2000US-0251030.
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2000US-0249245.
2000US-0249264.
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20000S-0251868.
20000S-0251869.
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2000US-0251990.
2000US-0254097.
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20000S-0249299.
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01 - DEC - 2000;
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2000US-0234997.
2000US-0234998.
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2000US-0233065.
2000US-0234223.
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2000US-0232399.
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2000US-0236369.
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2000US-0237040.
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2000US-0235834
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2000US-0236327
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                                                                                                                                                                                                                                                                                                                                                             SEP . 2000;
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20 OCF 2
20-0CI-2
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17 - NOV -
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) anto acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucieotides may be used in the prevention, diagnosis and treatment of discases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally. (1) polynucleotides may be used to product on of (1). Additionally. (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 concers from the present inwention. AAK5492 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoletic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ 1D NO 33324; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 22210 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCTGCG 22159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 52; DB 22; Length 29329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29329 BP; 6864 A; 6756 C; 7225 G; 8484 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.9e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein 5' EST, SEQ ID NO: 30024.
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                                                                                                                                                                                                                                                                                 Ruben SM
                                                                                                    2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251989.
2000US-025989.
                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                   2000US-0251030
2000US-0251988
                                                                   2000US-0256719
2000US-0251479
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Matches 52, Conservative
                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                 WPI; 2001-483426/52.
01-0EC 2000;
01-0EC-2000;
05-0EC-2000;
05-0EC 2000;
06-0EC 2000;
08-0EC 2000;
08-0EC 2000;
08-0EC 2000;
08-0EC 2000;
08-0EC 2000;
                                                                                                                                                                                          11 - DEC - 2000;
05 - JAN - 2001;
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AAC25949/c
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06-SEP-2000

2000US-0249300

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The invention relates to an isolated nucleic acid molecule (1) comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                         a nucleotide sequence us an isolated nucleic acid molecule (1) comprissing confication or its complement. (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer.

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate

cancer in a patient:

(d) assessing the efficacy of a therapy for inhibiting prostate cancer

in a patient:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1194 CCTTGGCCTCCCAAAGTGCTGGATTACAGGCATGAGCCACTGCGCCCAGC [HILL] [H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 51; DB 23; I
00.0%; Pred. No. 5.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Buman prostate expression marker cDNA 12942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monahan JE;
                                                                                                                                                                                                                                                  Claim 1; Page 674; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomic marker; gene; ss.
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Conservative 0
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200605-207454P.
200605-211314P.
200605-219007P.
200605-255281P.
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Schlegel R, Endege WO,
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                                                            WPI: 2001-662795/76
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Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40200160860-A2
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09-JUN-2000;
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13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is one of a large number of 5° ESTs derived from manAs encoding secreted proteins. No ORF has yet ineen conclusively identified within the present sequence. The 5° ESTs were prepared from footal human RNAs or polyA* RNAs derived from 30 different lissues. EST sequences usually correspond mainly to the 3° untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cubA libraries. Such ESTs are not well suited for isolating "CNA sequences have been obtained, the full 5° UTR is rerely included. 5° ESTs are derived from mRNAs with intuose cases where longer cDNA sequences have been obtained, the full 5° UTR is rerely included. 5° ESTs are derived from mRNAs with intuot 5° ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5° ESTS are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinoqen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in diagnostic, forensic, gene therapy and chromosome mapping procedures.
They are used to obtain upstream regulatory sequences and to design
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                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (% EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1194 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGT 1244
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[00.0%; Pred. No. 5.6e-13;
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                                                                                                                                                                                                                       Giordano J:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1: SEQ ID 30024; 71pp · CD-ROM: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 100.0%; Pred. No. 5.6
Conservative 0; Mismatches
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                                                                                                                                                                                                                       Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression and secretion vectors.
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                          21 FEB-2000; 2000EP-0200610.
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2000US-207454P.
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2000US-219007P.
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                                                                                                                                                                                                                    Dumas Milne Edwards J,
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ses 51; Conserv
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                                                                                                                                                       (GEST ) GENSET
                                                                                           26 - FEB - 1999;
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25-MAY-2000;
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Query Match
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                                                            The invention relates to an isolated nucleic acid molectic (I) comprising a nucleotide sequence given in Tables 1 9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human: prostate cancer; cytostatic; carcinogen; pharmac dyapamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                        (e) selecting a composition for inhibiting prostate camper in a patient;
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                                                                                                                                                                                                                     (1) assessing the prostate cell carcinogenic potential of a compound; (9) determining whether prostate cancer has metastusined in a pathent; (h) assessing the aggressiveness or indolence of prostale dencer in a
                                                                                                                                                                          (d) assessing the efficacy of a therapy for innubiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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 for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                     (1) is also useful as a pharmacodyanamic or pharmacoden mic marker.
                                                                                          specification or its complement. (1) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
                                                                                                                           (b) monitoring the progression of prostate cancer in a patient;(c) assessing the efficacy of a test compound to inhib: prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                 Sequence 159 BP; 87 A; 73 C; 71 G; 128 T; U other;
                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 23; 1
Pred. No. 5.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human prostate expression marker cDNA 13735
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                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                              Claim 1; Page 2136-2137; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABV1:744 Standard; cDNA; 366 BP
                                                                                                                                                                                                                                                                                                                                                                100.08;
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                 51: Conservative
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                                                                                                                                                             cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                            in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 - FEB - 2000;
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- 2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-Aug 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV13744:
                                                                                                                                                                                                                                                                      patient;
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13-DEC-
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    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (1) comprisis a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer.
                                                                                                                                                               (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
specification or its complement. (1) is useful for:
da assessing whether a patient is affilted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                            (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 51; DB 23; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 366 BP; 82 A; 96 C; 78 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 5.6e-13;
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20000S-189862P.
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20000S-219007P.
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Matches 51; Conservative
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                                                                                                                                      cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200160860-A2
                                                                                                                                                                                                         in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-FEB-2000;
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25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-DEC-2000;
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Gaps

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. DB 22; L 5.6e-13;

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Conservative

1.8%; Score 51; 100.0%; Pred. No.

Length 396

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Seguence 396 BP; 124 A; 75 C; 87 G; 110 T; 0 other;
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Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                ABV34857
                                                                                                                                                                                                                                                                                                          The invention relates to human polymucheotines (AA17941-AA19441) and the encoded proteins (AA000010-AA018910) that exhibit arrivity elating to cytokine, cell proliferation or cell differentialism or which may induce production of other cytokines in other cell, populations. The polymucheotides and polymetides are useful in generating the rappy practices or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            populde therapy. The polypeptides have various cytoking like activities, e.g. stem cell growth factor activity, haemstopologis conducting activity activity, tissue growth factor activity, immunosopilatory activity and
                         in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arthritis and
                     (e) selecting a composition for inhibiting prostate cannot in a patient
(f) assessing the prostate cell carchinogenic potential of a compound;
(d) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                Gaps

    is also useful as a pharmacodyanamic or pharmacogeness markers.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activin/inhibin activity and may be useful in the diadress and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosing and treating e.g. Leukaemia, inflammation and immune
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                                                                                                                                                                                                                                                                                         1194 PCITGGGCTCCCAAAGIGCTGGGATTACAGGCAIGAGGCACIGGCCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of cancer, leakaemia, nervous system disorders
                                                                                                                                                                                                                                                                                                            indels
                                                                                                                                                                                                       DB 23; Length
5.6e-13;
                                                                                                                                                                   Sequence 381 BP, 81 A, 103 C, 86 C, 111 T, 0 other:
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                                                                                                                                                                                                       Match 1.8x; Score 51; DH 1. Decal Similarity 100.0%; Pred. No. 5.6c es 51; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polynucleotide SEQ 1D NO 1713.
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18 MAY-2000: 2000US-0577409
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Matches
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(a) assessing whether a patient is diffracted with prostate rancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene: ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                          1.8%; Score 51; DB 23; Length 406.
100.0%; Pred. No. 5.6e-13;
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1187 CTGCCCACCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGC
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-211314P.
-219607P.
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2006US-189862P.
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200000S-2
20000US-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in a patient;
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16-MAR-2000;
25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 - FEB - 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                     ABV34857;
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ABV42939 standard; cDNA; 412
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                                                                                                                                           Homo sapiens
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13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                 Schlegel R,
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ID AA1879
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AC AA1879
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DI 06-NOV
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ABV42939
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(a) assessing whether a patient is afficient with position of the progression of prostate cancer:
(b) monitoring the progression of prostate cancer in a patient.
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound:
                                                                                                                                                                            Human, prostate cancer, cytostatic, carcinoqum, pharmac Jyanafic marker; pharmacogenomic marker, gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (4) determining whether prostate cancer has metastasized in a patient:(b) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (d) assessing the efficacy of a therapy for schibiting prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1194 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCACTGCGCCCACACT 1244
 1194 CUTTGGCCTCCCAAAGTGCTGGGATTACAGGGATGAGCCACTGCGCCCAGC 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 CCTFGGCCTCCGAAAGTGCTGGGATTAGAGGCATGAGCCACTGGGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,56-13;
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Pred. No. 5.5e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 100.0%; Pred. No. 5.5v
51; Conservative 0; Mismatches
                                                                                                                                                      Human prostate expression marker cDNA 34064.
                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Monahan JE;
                                                                                 ABV34073 standard; cDNA; 412 BP
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer in a patient;
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Best Local Similarity
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                                                                                                                                                                                                                  Homo sapiens
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25-MAY-2000;
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                                                           RESULT 31
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(a) assessing whether a patient is affilicted with prostate cuncer:
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the adgressiveness or indolence of prostate cancer in a patient.
                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
pharmacogenomic marker; gase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (d) assessing the efficacy of a therapy for inhibiting prostate cancer
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%; Score 51; DB 23; Length 412;
100.0%; Pred. No. 5.6e-13;
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                                                           Human prostate expression marker cDNA 42930.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-189862P.
2006US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 2001-662795/76.
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25-MAY-2000;
09-JUN-2000;
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20-FEB-2001; 2001WO US05171.
WO200160860-A2.
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                                                                                                               16-MAR-2000;
25-MAY-2000;
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18-JUL-2000;
                                                                                                                                                                                     13-DEC-2000;
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                                23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human polynucleotides (AA17994, AA19484) and the encoded proteins (AA000010-AA01995) that exhibit arrivity elating to reprokine, cell proliferation or cell differentiation on which may induce production of other cytokines in other cell populations. The polyneteotides and polypeptides are mental in seek therapy, vaccines or peptide therapy. The polypeptides have various cytoxine like activities, e.q. stem cell growth factor activity, hammalopolesis remulating activities activity, issue growth factor activity, immunomode and or activity and activity and may be useful in the diagnosts and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from KIPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; prostate cancer; cytostatic; carcinoaen; pharmac Jyanamic marker;
                                                  gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           School
                                              Human: cytokine; cell proliferation; cell differentiation, gene that vaccine; peptide therapy, stem cell growth factor, haemalopolesis; tissue growth factor; immunomodulatory; cancer; lenkaemin; hervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acids and polypeptides, useful for projection diagnosing and treating e.g. leukaemia, inflammation and usmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human prostate expression marker conn 43794
                polynuclectide SEQ ID NO 8018
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                                                                                                                                                                                                                                                                    28-FEB-2000; 2000US-0515126.
18-MAY:2000; 2000US-0577409
                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927
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                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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                                                                                                                                                                 W0200164835-A2.
                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation.
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                Human
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The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 19 (ABW0010-ABW62213) of the specification or its complement. (1) is useful for:
(a) assessing whether a patient is afflicted with prostate rance;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prestate cancer in a patient.

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) defermining whether prostate cancer has metastasized in a patient;
    (h) assessing the agressiveness or indolence of prostate cancer in a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated mucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 8714; 11750pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     Monahan JE;
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                                                             2000us-183319P.
2000us-189862P.
2000us-207454P.
2000us-211314P.
2000us-219007P.
20-FEB-2001; 2001WD-US05171
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Monahan JE;

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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                             Endege WO,
                                                  WPI; 2001-662795/76
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                             Schlegel R,
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                                                                                                                                                                                                                                                                                    patient
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 37
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                                                                                                                                                                                                                                                                                                       (e) selecting a composition for inhibiting prostate cancer in a patient: (t) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient:
                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful tor detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                          assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                       The invention relates to an isolated nucleic acid molecule (1) comprise a nucleotide sequence given in Tables 1-9 (ANY00010-ANV622.3) of the appendication or its complement (1) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer:
(b) monitoring the progression of prostate cancer in a patient:
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                .8%; Score 51; DB 23; Length 645; 0.0%; Pred, No. 5.6er/13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 446 BP; 108 A; 112 C; 96 G; 127 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%; Pred. No. 5.6.
Matches 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cONA 2950.
                                                                        (MILL.) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                               Monahae JE:
                                                                                                                                                                                    Claim 1; Page 799; 11750pp; English.
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2000US - 207454P
2000US - 211314P
2000US - 219007P
2000US - 255281P
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     2000US - 189862P.
2000US - 207454P.
2000US - 211314P.
2000US - 219007P.
2000US - 255281P.
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                                                                                             Endege WO.
                                                                                                                    WP1: 2001-662795/76.
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18-JUL-2000;
13-DEC-2000;
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25-MAY-2000;
                                                                                                                                                                                                                                                                                                in a patient;
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                                                  13 DEC: 2000;
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        16-MAR-2000;
                 25-MAY-2000;
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                              JUN-2000
                                       18-JUL-2000;
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                                                                                               Schlegel
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ABV02959
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the elficacy of a test compound to inhibit prostate cancer in a patient.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (e) selecting a composition for inhibiting prostate cancer in a patient;
Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                     (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;

    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%; Score 51; DB 23; Length 459;
00.0%; Pred. No. 5.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGGCATGAGCGCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. nc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                    Claim 1; Page 549; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmacogenomic marker; gene; ss.
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20000S-207454P.
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2000US-219007P.
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Matches 51; Conservative
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18-JUL-2000;
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25-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200160860-A2
                                                                                                                                                                                                             in a patient;
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                                                                                                                                                                                                                                                                                                                                     patient
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                                                                                                                                                          The invention relates to an isolated nucleic acid colect (1) comprising a nuclectide sequence given in Tables 1.9 (ABV30010-ABV*2213) of the specification or its complement. (1) is useful four (2) the sessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer is a refient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                (e) selecting a composition for inhibiting prostate cannet in a patient; (f) assessing the prostate cell carcinogenic peterlaise, or a compound; (g) determining whether prostate cancer has metastassassing in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, prostate cancer, cytostatic, carcinogen; pharmacodyanamic marker,
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prostate cells and correlating with presence of prostate cancer, useful
                 prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, useful
                                                                                                                                                                                                                                                                                                                                     (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                    Novel isolated nucleic acid molecule associated with carrerous state
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (1) is also useful as a pharmacodyanamic or pharmacogenteld marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lougth 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 512 BP; 118 A; 136 C; 114 G; 144 T; 0 other;
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hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 51; DB 24;
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tive 0; Mismatches
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                                                                                                               Page 7297-7298; 11750pp; English
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2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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Matches 51, Conservative
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                                                                                                                                                                                                                                                                                                                cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                              in a patient;
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09-JUN 2000;
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                                                                                                                    Claim 1;
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(a) assessing where a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient.
The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is affiliated with prostate cancer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                                                                                                                                                                                                                                     (e) selecting a composition for inhibiting prostate cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                                         determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                               (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                  (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                    (b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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5.6e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 51;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 8698; 11750pp; English.
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Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer;
pharmacogenomic marker;
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(a) assessing whether a patient is affliced with prostate cancer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human: prostate cancer; cytostatic; carcinoqen; pharmachiyanamic marker; pharmacogenomic marker; qene; ss.
                                                                         a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with careforus state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

    (c) selecting a composition for inhibiting prostate carret in a patient
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized on a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

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in a patient;
                                  (d) assessing the efficacy of a therapy for inhibiting prostate cancer
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(1) assessing the prostate cell carcinogenic potential of a compound:
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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 assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                    255 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGG 305
                                                                                                                                                                                                                                                                                               1194 CCTTGGCCTCCCAAAGIGCTGGGATTACAGGCATGAGGCACTGCGGCCAG:
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                 Length
                                                                                                                                                                                           Sequence 515 BP: 118 A; 135 C; 115 G; 146 T; 1 other;
                                                                                                                                                                                                                             DB 23; L
                                                                                                                                                                                                                             ch 1.8%; Score 51; DB il Similarity 100.0%; Pred. No. 5.6 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate expression marker conA 32637
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-2119007P.
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                    cancer in a patient;
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09-3UN-2000;
18-JUL-2000;
                                                       a patient;
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pharmacogenomic marker; gene: ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (d) assessing the efficacy of a therapy for inhibiting prostate cancer
in a patient;
   has metastasized in a patient;
                                                                                                                                                           Gaps

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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(a) assessing whether a patient is affilted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient.

    is also useful as a pharmacodyanamic or pharmacogenomic marker.

(9) determining whether prostate cancer has metastasized in a pat(h) assessing the aggressiveness or indolence of prostate cancer
                                                                                                                                                           0;
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                                                                                                                                                                                          1194 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCCAGC
                                                                                                                         Length
                                                                                     Sequence 521 BP: 119 A: 138 C: 118 G: 146 T; 0 other;
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                                                                                                                    Query Match 1.8%; Score 51; DB 23; I
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0;
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2000US-211334P.
2000US-219007P.
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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                                   patient;
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Sequence 521 BP; 119 A; 138 C; 118 G; 146 T; 0 other;

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250 CCTTGGCCTCCCAAAGTGCTGGATTACAGGCATGAGCCACCAGC 300
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ABV21487
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(a) assessing whether a patient is affiliated with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient.
(c) assessing the efficacy of a test compound to inhibit prostate
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(d) assessing the efficacy of a therapy for inhibiting prostate cancer
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                                                   Gaps
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                                                                                CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGGCCCAST 1244
                                                                                               1.8%; Score 51; DB 23; Length 521;
100.0%; Pred. No. 5.6e-13;
                  Length 523;
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                 1.8%; Score 51; DB 23; 100.0%; Pred. No. 5.6e-13;
                                                                                                                                                                                                                                                                                             Human prostate expression marker conn 42187
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Rest Local Similarity 100.08; Pred. No. 5.00
                         100.0%; Preu. ...
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2000US-207454P.
2000US-211314P.
2000US-219007P.
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                                Best Local Similarity 100.
Matches 51: Conservative
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25-MAY-2000;
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                    Query Match
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1194 CCTTGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGGGCCCACT [244

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                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient:

(c) assessing the efficacy of a test compound to inhibit prostate
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Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 51; Conservative 0; Mismatches 0;
                                                             Human prostate expression marker cDNA 43741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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                                                                                                                                                          pharmacogenomic marker; gene; ss
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2000US-207454P,
2000US-211314P,
2000US-219007P,
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                                                                                                                                                                                                                                                                                        W0200160860-A2
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18-JUL-2000; 2
13-DEC-2000; 2
                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000;
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16-SEP-2002
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Human prostate expression marker cDNA 21901
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                            Homo sapiens.
                                                                                                                               20-FEB-2001;
                                                                                                                                                      17-FEB-200G;
                                                                                                                                                                                                                                                                 Schlegel R,
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D.E.
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(a) assessing whether a patient is affilicated with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (e) selecting a composition for inhibiting prostate caper. Is a patient, (1) assessing the prostate cell carcinogene polential or a compound (1) determining whether prostate cancer has merasised a patient (3) determining whether prostate cancer has merasised a patient (b) assessing the aggressiveness of indolence of prostate cancer in a
                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmar-lyacamic marker;
pharmacogenomic marker; gene; ss.
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    is also useful as a pharmacodyanamic or pharmacogeneous market.

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                                                                     duman prostate expression marker cDNA 2:478
                                                                                                                                                                                                                                                                                                                 (MILL:) MILLENNIUM PREDICTIVE MEDICINE INC
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ВР
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2000US-207454P.
2000US-211314P.
2000US-219007P.
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AHV21487 standard; cDNA; 670
                                                                                                                                                                                                     20-FEB-2901; 2001WO-US05171.
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Matches 51: Conservative
                                                                                                                                                                                                                                                                                                                                         Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer in a patient;
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                                                                                                                                                                                                                                       16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a patient;
                                                                                                                                                                                                                                                                           18-JUL-2000;
                                                                                                                                  domo sapiens.
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                                                                                                                                                                                                                                                                                                                                        Schlegel R,
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                                             13-SEP-2002
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The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (1) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer:
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (t) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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    is also useful as a pharmacodyanamic or pharmacogenomic marker.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8%; Score 51; DB 23; Length 670; 100.0%; Pred. No. 5.6e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monahan JE;
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2000US-207454P.
2000US-211314P.
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Best Local Similarity 100.0%
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16 - MAR-2000;
25 - MAY-2000;
09 - JUN-2500;
18 - JUL-2000;
                                      09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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        17-FEB-2000;
                 16-MAR-2000;
25-MAY-2000;
                                                                                                       Schlegel R,
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                                                                                                                                                                                                                                                                                   comprising
                                                                                                                                                                                                                                                                                                                                                                                  (e) selecting a composition for inhibiting prostate cancer in a patient;(f) assessing the prostate cell carcinogenic potential et a composid;(a) determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; currimogen; poutmas; quoumne marker; pharmacogenomic marker; qene; ss.
                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate ceils and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                            (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                    (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SdpS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (1) is also useful as a pharmacodyanamic or pharmacogen. To market.
                                                                                                                                                                                                                                                                                                      specification of its complement. (1) is useful for:
(a) assessing whether a patient is afflicted with prostute cancer.
(b) monitoring the progression of prostate cancer in a patient:
(c) assessing the efficacy of a test compound to inhibit prostate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker conv 22443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                  (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                             Claim 1; Page 3919-3920; 11750pp; English
                                                                                                                                                                         Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARV22952 standard; cDNA; 670 BP
                                                                                  2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-2190U7P.
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                                                   2001WO-US05171.
                                                                         2000US-183319P.
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                                                                                                                                                                         Endege WO,
                                                                                                                                                                                                                                                                                                                                                    in a patient;
                                                                                                                                                                                             WPI; 2001-662795/76
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                                                                                                                   18-JUL-2000;
13-DEC 2000;
                                                   20 - FEB - 2001;
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                                                                        17 FEB-2000;
                                                                                   MAR-2000;
                                                                                              MAY - 2360;
                                                                                                        09-JUN-2000;
                                                                                                                                                                        Schlegel R,
                             23 - AUG - 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; qene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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100.0%; Pred. No. 5.6e-13;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                          (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                                                                                                                                                                                                                       Monahan JE:
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200,08+189862P.
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                           2000US-389862P.
2000US-207454P.
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2000US-219007P.
2000US-183319P
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Matches 51: Conservative
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The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                                                                                                                                                                                                  (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                         Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, usef for detecting presence of prostate cancer.

    is also useful as a pharmacodyanamic or pharmacogenomic marker

                                                                                                                                                                                                                                                       (b) monitoring the progression of prostate cancer in a patient;(c) assessing the efficacy of a test compound to inhibit prostate
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00.0%; Pred. No. 5.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 670 BP; 164 A; 167 C; 146 G; 190 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 28291.
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                                                                                                                             Claim 1; Page 5697 5698; 11750pp; English.
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2000US-207454P.
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                                                                                                                                                                                                                                                                                                 cancer in a patient;
WPI; 2001-662795/76.
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Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                           in a patient;
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25-MAY-2000;
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13-DEC-2000;
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      Ö
                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid molecule (1) comprising a nucleotide sequence given in Tables 1.9 (ABV)0010-ABV02213) of the specification or its complement. (1) is useful to:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a Fallent;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potentia; or a compound; (g) determining whether prostate cancer has metastas zer in a patient; (h) assessing the aggressiveness or indolence of prostate cancer. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytoStatin; carolisator; pourman fyanamic marker; pharmacogedomic marker; gene; ss.
                                                                                                                                                                     Novel isolated nucleic acid molecule associated with pare-cous state of prostate cells and correlating with presence of prostate cancer, asetulion detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (d) assessing the efficacy of a therapy for inhibiting prustate cancer
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100.0%; Pred. No. 5.6e-13;
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                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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                                                                                        Monahan JE:
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Best Local Similarity 100.0
Marches 51, Conservative
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                                                                                      Schlegel R,
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Ciaim 1: Page 5888: 11750pp: English.

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                                        The invention relates to an isolated nucleic acid molectic (T) comprising a nucleotide sequence given in Tables 1-9 (ABW00010-ABW2213) of the specification or its complement. (T) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer:

(b) monitoring the progression of prostate cancer in a fullect;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cancer has metastasized in a patient;

(f) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
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    is also useful as a pharmacodyanumic or pharmacogenesic sarket.

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Hest Lorai Similarity 100.0%; Pred. No. 5.569 [3]
Matches 51; Conservative 0; Mismatches 0; Indo-Ex
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Search completed: May 9, 2003, 19:01:43 Job time : 1750.62 secs

B1059823 IL3-UT011 B1015195 MR4-ET014 B6745912 602724092 B6014649 11.5-GN023	BG007260 IL5-GN023 AQU56873 CIT-HSP-2	AA10265 z109e05.s BF431825 nab50h08. AW104031 xd64a05.x BG576148 602587119	AQ663862 HS_2151_B A1610607 tp19q09.x B1062371 LL3-UT011 B710918 id34q04.y	BI711369 id94q04.x AI264119 qi08h11.x BM730147 ij53f05.y	AA481408 zv02g09.s AI679442 tu63h07.x	A133/Ub5 qx82911.x A1679952 tu67h07.x H1062368 IL3-UT011	AI089524 oz22a01.x AI002969 an23903.s SQ007739 UI-H-EI0-	AQ48'571 RPCI-11-2 AW971724 EST383813 AQ623696 HS_5319_A	AIO84593 CX63f01.S AQ589333 CITBI-E1- AV718287 AV718287	AQ198714 RPC111-59 AA662976 ac52b01.s H90008 yu83d03.s1	AA486970 ab17f12.r BF924753 CM1-NT020 AQ280600 CITBI-E1-	AQ178114 HS_2217_B #58672 yr20d05.s1	AQ334511 HS_5011_A AQ342716 RPC111-11	A(912852 CZZUDUS.X AQ395413 CITBI-EI- AQ260373 CITBI-EI-	AQ586921 RPC1-11-4 BE062160 RC1-BT025 A1767338 DKE7E6861	AA004719 zh95b06.s AQ937500 NB6-1040R	AG175929 Pan trogl AG085391 Pan trogl	AG183007 Pan trog1 BQ880055 AGENCOURT AOR39852 2601.13-C5	R48131 Yj66a12.rl AQ296069 HS_3080_A	H16875 ym34f04.rl BE972845 601652083 BC015976 Homo sabi	BM722770 U1-E-E00- AG059141 Pan trog1	AQ394009 CITBI-EI- AG053850 Pan Lrog1	B1259846 6029/1503 BG385823 602454059	.BF674499 60213/2// BQ926504 ACENCOURT BF526040 602071145	AL537956 AL537956 H64265 yr70dll.rl	AQ49U63Î RPCI-11-2 A£926104 WO42d11.x
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GenCore version 5.1.5 Copyright (c) 1993 - 2003 Compugen Ltd	c search, using sw model	9, 2003, 16:20:31 ; Se	US-09-846-456-3 2893 1 acayggcatggtggcaggtg	OL.IGO_NUC Gapop 60.0 , Gapext 60.0	16154066 seqs, 8097743376 residues		<pre>iotal number of hits satisfying chosen parameters: Minimum DB seq length: 0 MAX:mum DB sex length: 0</pre>	Post processing: Listing first 1000 summaries	-	em_esthum:* em_estin:* em_estmu:*	em_estpl:# em_estpl:# em_estro:#	em_htc:* qb_est1:* qb_est2:*			em_estom:* qb_gss:* em_gss_bum:*			em_gss_mas:* em_gss_mus:* em_gss_other:*	em_gss_pro:*	results predi to the score	d by analysis of the total scor	SUMMARIES	oueny Match Length DB ID	.4 289	.0 617 10 .0 219 17	.0 424 9 .0 674 17
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467 bp mRNA linear EST 21-AUG-1997 ng37702.s1 NCI_CGAP_CO3 Homo sapiens cDNA clone IMAGE:936962 3'', AA527406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"Organ: breast, Vector: pucl8: Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ONESIES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
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                                                                                                                                               Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Frobect. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6st2=RC6-BT0252-271099·012-ci0at3+1999·10-27at4=1)
Seq primer: puc l8 forward
High quality sequence start: 146
High quality sequence stor: 289.
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Email: cqapbs:f@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.
, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo,
1 (bases 1 to 467)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Fax: +55-11-2707001
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Matches 126; Conservative
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PMO-HT0608-170300-001-f02 HT0608 Homo sapiets CENA, mHNA sequence.
BE178833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anote-TVector: pr773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco F: 1St strand cDNA was prepared from 12 pooled bulk tamot samples and primed with a Not I - Oligo(AT) primer. Double stranded cDKA was ligated to Eco RI adaptors (Pharmacia), divested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library went through one round of normalization.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao PaulorSP,
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                insert Length: 1057 Std Error: 5.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 380.
Location/Qualifiers
ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                            /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:98692"
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Laboratory of Cancer Genetics
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/organism-"Homo sapiens"
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/clonc_lib-"Hr0608
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/dev_stage="Adult"
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Sma1:
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/incle="Croan: head_neck; Vector: puc18; Site_1: Sma1: Sm
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RPCI-11-343L18.TJ RPCI-11 Homo Sapiens genomic clone RPCI-11-343L18
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 219)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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Map Building
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RPCIll Human Male BAC Library"
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Clones are derived from the human BAC library RPCI-11. For BAC
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Other GSSs: RPC1-11-343L18.TV
Other GSSs: RPC1-11-343L18.TV
Contact: Snaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cyapbs-famil.inih.go.
Tissue Procurement: W. Marston Linehan, M.D., Schlige Chidqui. M.D., Michael Emmert-Buck, M.D., Ph.D.
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Eukaryota, Metazoa, Chordata: Craniata: Vertebra'u, Euteleostomi;
Mammalia; Eutheria, Primates, Catarrhini; Homiciiue; Homo.
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National Cancer Institute, Cancer Genome Anatomy Froject (CGAP),
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HJ059823 569 bp mRNA linear EST 15-JUN-2001
1L3-UT0115-G80101-378-H06 UT0115 Homo sapiens CDNA, mRNA sequence.
HJ059823
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Jusa Neto, E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Krustein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Sharres,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
                                                                                                                                                                                    Pan troalodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male BAC Library clone:PTB-057L02.R.
Pan troalodytes
                        3SS 03-NOV-2001
AGUB/644 13S 03-NOV-200 PAR Linear 3SS 03-NOV-200 Pan troqlodytes DNA, clone: PTB-057L02.R, genomic survey sequence. AG067644
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Totoki,Y., Watanabe.H. and Sakaki,Y.
BAC end sequences of Library PTB
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/clone_lib-"PTB Chimpanzee Male BAC Library"
i 162 c 179 g 179 t 2 others
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1. 674
/organismr*Pan troglodytes*
/db_xref-*Laxon:9598*
/clone-*PTB-0571.02.R*
/sex-*male*
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Matches 57, Conservative
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R.Site 2
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/note=Torgan: uterus_tumor; Vector: purit; Site_1: Smaj:
Site_2: Smal; A mini-tibrary was made by cloning products
derived from ORESTES PCR (U.S. Letters Sarent application
No. 196,716 - Ludwig Institute for Carver Research)
profiles into the PUC 18 vector. Reyerse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions:
114 - 119 - 151 t
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Enkaryota: Metazoa; Chordata; Craciata; Vertebratu, Estelenstomi;
Mammalia: Eutheria; Primates; Catarrhini; Hamiticae: Homo.

1 (bases 1 to 600)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeidu,S., Britches,M.R., Nagai,M.A., da Silva,M. Jr., Zaqo,M.A., Batulin,S., Gusta,F.E.,
Brunstein,A., deoliveira,P.S., Bucher,P., Gorgenerol,C.V., O'Hare
JM.J., Soares,F., Brentani,R.R., Reis,L.F., de Solza,S.J. and
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PRNA sequence.
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This sequence was derived from the FAPESP/LICK Furst Cancer Genome Project. This entry can be seen in the following TRL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl="Likt2-TL3 U:0115-C8C:01-378-H06&t3-2001-09&t4-1]
Seq primer: puc 18 forward
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509 01., Suo Paulo-SP.
                                                                                                                                     Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 21509-7∂0. Sao Paulo-SP,
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Shotgun sequencing of the human transcriptome with ORF expressed
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ilarity 100.0%; Pred. No. 1.1e-10;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone_lib="UT0115"
/dev_stage="Adult"
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Location/Qualifiers
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                                                                                            Contact: Simpson A.J.G.
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI: Site_2:
Ecori: cDNA made by Oligo-dr priming. Directionally cloned
into Ecori/XhoI sites using the following 5 adaptor:
GGAGGAG(G). Library constructed by Ling Hong in the
aboratory of Gerald M. Rubin (University of California,
Herkeley) using APP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwing.org.br/Scripts/gethtml2.pl?tl-MR4.t2-MR4.ET0140-190201-006-e12413-2001-02-196.t4-1)
Seq primer: puc 18 lorward
High quality sequence start: 18
High quality sequence stop: 72.
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Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Futheria; Primates; Catarrhini; Hominidae: Homo.
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Clone distribution: MGC clone distribution information can be
Clone distribution: MGC clone distribution information can be
Clound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1691 row: h column: 24
High quality sequence stop: 841.
Location/Qualiflers
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NIH-MGC http://mgc.nci.nib.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: egapbs-remail.nih.gov
Email: egapbs-remail.nih.gov
Ensure Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/db_xref="taxon:9606"
/clone="IMAGE:4850375"
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/db_xref="taxon:9506"
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/note=lorgan: placenta_normal; Vector; paci8; Site_1: Stall Site_2: Smal; A mini-illerary was made by cloahing products derived trom (MESIBS PTR (0.5, Letrers Paten: application No. 196,716 | indayig institute for Cancer Research) profiles into the pUC IN vector; Reverse transcription of tissue mRNA and cONA amplification were performed under low stringency conditions.
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1 (bases 1 to 384)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Bricnes,M.R., Nagal,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Hadia,S.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Hucher,P., Jongener,L.C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de S.u.za,S.J. and
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IL5-GN0239-211200-342-907 GN0239 Homo sapiens chAA, mkNA seguence.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 21509-510, Sao Paulo SP.
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NIH_MGC Library.
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Diss Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Magai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jorgeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
                            ысии/260
TLS-GN0239-271100-281-e06 GN0239 Homo sapiens cDNA, mRNA sequence.
BG007260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson/ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl~LL5&t2~LU5-GN0239-271100-281-e06&t3~2000-11-27&t4-1)
Seq primer: puc 18 forward
                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/dev_stage="Adult"
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Chissoo, S., Dietrich, N., DaBuquert, Fawellow, M.E., Thispellish, Hawkins M., Huttman, M., Kucaba, T., Lawy, M., Tew, M., Tew, M., Martis, E., Moore, S., M., Morris, M., Parsons, J., Prange, C., Kirkin, M., Morling, T., Schellenberg, K., Soares, M.B., Tanck, Thierry-Met., I Previses, E., Underwood, K., Wohldmarn, P., Waterston, R., M. Isson, N. and Marra, M. Generation and analysis of 286, DP, Lumqu excressed anguence Tasks. Generation and analysis of 286, DP, Lumqu excressed anguence Tasks.
                                   Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Fass, S., Timber, K., Solden, K., Berry, K., Granger, D., Suh, E., Kible, T., Shizuya, H., Simon, M. and Wenter, J.C.
Use of a randow BAC End Sequence Database for Schence-Ready Map Building (1998).
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Seg primer: M13-21
Eukaryota, Metazoa, Chordata, Craniata, Vertebia'u, Eute.costomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
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4444 Forest Park Parkway, Box 6:65, St. Louis, Serfice
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                                                                                                                                                           Outhorished (1998)
Other GSSs: CIT-HSP-2339H7.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockwille, MP 200450, 958
The: 301 838 0208
Email: mdadams@tigr.org
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/db_xref="taxon:9606"
/clone="2339H7"
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100.0%; Pred. No.
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/sex="Male"
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/sex_male.../dow.kevpost conception fetus.../dow.stage...20 week-post conception fetus.../dow.stage...20 week-post conception fetus.../dow.stage..../dow.stage...
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Mammalia: Eutheria, Primates: Catarrhini; Hominidae: Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer institute, Cancer Genome Anatomy Project (CGAP),
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This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1517—Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 274.
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//nth.mestratin project Vector: pI7T3D-Pac (Phatmacia) v
//nth.mestratin project polytics site]: Not I; Site 2: Eco MI;
Papad: amounts of plasmid DNA from five normalized
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AACTSGAAGAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
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/.ab_test "DH1UH"
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Unpublished (1997)
Contact: Fobert Stransberg, Ph.D.
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/db xret "taxon:9696"
/c.ome-"IMAGE:3269606"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:430304"
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us-09-846-456-3.oli30.rst

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Following HAP purification, this DNA was used as tracer is a subtractive hybridization reaction. The fiver was PCR-amplified cDNAs from pools of 5.0% clones made from the same 5 libraries. The pools consisted of the following libraries and clonebus: Soares NBMSF pro. i. 309384-310919, 323208-325895 Soares NBMSF pro. i. 145032-147335, 147720-148103, 148872 14725, i5002 - 150407, 15115-15232 Soares NBMSF pro. ii. 304776-15232 Soares NBMSF pro. ii. 304776-306311, 320136-322823, 326280 states NBMS pro. ii. 758280-760513, 773084-74407 Soares NBMS pro. ii. 304776-306311, 320136-322823, 326280 states of the following soares and M. Fatima Bosaldo." 739080-74095 Surfraction by Hento Soares and M. Fatima Bosaldo."
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Contact: Robert Strausberg, Ph.D.
Email: CapbS-remail.nih.gov
Ilssue Procurement: Christopher Moskaluk, N.D., on B., Michael R.
Emmert Buck, M.D., Ph.D.
CSNA Library Preparation: Life Technologies, Inc.
CSNA Library Arrayed by: Greq Lorence, Ph.C.
LNA Sequencing by: Washington Toiversity Preparation: N.S.
Clone distribution: N.S. Coffe close distribution: N.S. Cound through the I.M.A.G.E. Consorts my New Residention and by
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//tissue_type**Tumor. 5 parted (see description)*
/lab_host="DHIGH"
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NCT-CGAP http://www.ncbi.nlm.nih.gov/nc?cqap.
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100.0%; Pred. No. 7.8e-16;
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Seq primer: -40UP from Gibco
High quality sequence stop: 424.
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Lengarh S. S.

Pred. No. 7.1e (0)

100.08;

Best Local Similarity 100.8 Matches 54, conservative

guery Match

U: Mismaiches

1.98; Score 54: 18 16;

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AC663862 453 bp DNA Linear GSS 23-JUN-1999 4S_2151_BL G10_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2151 Col-19 Row-N, DNA sequence. AQ663862.1 GL:5171630
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Mahairasis s. Wallace, 177, Smith, K., Swartzell, S., Holzman, T.,
Kelleria, Shakei, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                           BG575148 1inear EST 10 APR-2001 602597119F1 NIH_MSC.87 Homo sapiens cDNA clone IMAGE:4705901 57,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia: Entheria: Primates, Catarrhini, Hominidae, Homo,
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1 (bases 1 to 814)
11 HMC http://mgc.nci.nih.gov/,
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab_host_forlab (phage=resistant)"
/note="organ: breast; vector: pcNV-5PORI6; Site_l: NotI:
Site_2: Sali; cloned unidirectionally; oliqo-dT primed.
Average insert size 1.383 kb. Library enriched for
full: length clones and constructed by Life Technologies.
Note: this is a NH-MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The LiM.A.S. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMI057* row: e column: 06
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Best Loral Similarity 160.0%; Pred. No. 5.1e-10;
Matches 54; Conservative C: Mismatches O; Indels
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/clone_lib="NIH_MGC_87"
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Location/Qualitiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Lissue Procurement: DCTD/DTP
                                                                                                                                                                                               mRNA sequence.
BG576148
BG576148.1 GI:14583801
ESI.
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tpl9g09.x1 NCI_CGAP_Gas4 Home Sapiens cGNA clone (MAGE:2183288.37 similar to TR:099634 G09634 RIG-6. [1] ;centains Alm repetitive element, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausbers, Ph.D.
Email: cgapbs-remail.cih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Fr.D., Michael R.
Fismert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Gred Lemon, Ph.D.
DNA Sequencing by: Washington University denome Sequencing Conter
Clone distribution: MCI-CGAP clone distriction ran be
tomid through the I.M.A.G.E. Consortion/LML at.
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Mammalla, Eutheria, Primates, Catarrhini, Homin, Lies Romo.
1 (bases 1 to 658)
NCI-CGAP http://www.ncbi.nlm.nih.qov/ncicqqs.
National Cancer Institute, Cancer Genome Acatory Fruject (GGAP),
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BAC end Web Server: http://www.htsc.washing.co.com
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/clone="Plate-2151 Col-19 Row-N"
/clone_lib="CIT Approved Human Genemic sperm Libiary In"
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                      Sequence-tagged connectors: A sequence approact.
                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 96169,
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.8%; Score 53: DB 17; 100.0%; Pred. No. 1.7e-59:
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Insert Length: 2270 Std Erro:: 6.00
Seg primer: -400P from Gibeo
High quality sequence stop: 372
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1. .658
                                         scanning the human genome
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Unpublished (1997)
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(bases 1 to 23)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Najai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.E., Goldman,G. H., Carvalho,A. F., Matsukuma, A., Bala,G.S., Simpson,D.H., Brunstein,A., de:)liveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soofes,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson, A.J., Sago,M.J., Soofes,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Shotgun sequencing of the human transcriptome with OKF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3·Uf0117-160301-502-ED0_1&t3*-2001-03-16&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 15-JUN-2001
                                                                                                                                                                                       /note-"Organ: stomach, Vector: pcMV-SPORT6; Site_1; Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Motazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/ordanism-"Homo sapiens"
/db_xref-"taxon:9606"
/rlone-"IMAGE:2188288*
/rlone_lib-"NC!_CGAP_Gas4"
/issue_type-"poorly differentiated adenocarcinoms with signer ring cell features"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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/db_xref-"taxon:9606"
/clone_lib="UT0117"
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/tissue_type='insulinona"
/tissue_type='insulinona"
/tissue_type='insulinona"
/lab.ost='DHIGB (phage-resistant)"
/note='Organ pancreas; Vector: piluescript SK-; Site_l:
Xhol; Site_2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo cass excised to
pBluescript SK- by Dr. H. Incue tollowing the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
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Library was constructed by Dr. J. Ferrer In vivo cass-excised to
Library was constructed by Dr. H. Inoue DMA sequencing typ Washington
University Genome Sequencing Center For incommute, not obtaining a
clone please contact: Dr. Hitoshi Inoue (hinoue-sectional).
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Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Bichody, 7 Divinity Ave. Cambridge,
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Contact: Douglas Melton, Klaus H. Kaestner, & Hillost, Inoue
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Mammalia, Eutheria, Primates, Catarrhiul, Hominidac, Homo,
1 (bases 1 to 249)
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High quality sequence stop: 190.
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Matches 52; Conservative
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Library was constructed by Ur. J. Ferrer In vivo mass-excised to
Library was constructed by Ur. J. Ferrer In vivo mass-excised to
pBlueScript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact. Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Possible reversed clone: similarity on wrong strand
Seq primer: -40up from Gibco
High quaitty sequence stop: 316.
Location/Qualifiers
1.348
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 348)
Metton, D. Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Cilfton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Formitt, A., Theusing, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M. McCann, R., Cole, R., Tsagarelshvili, R., Williams, T.,
Jackson, Y., and Bowers, Y.
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Dept of Molecular and Cellular Blology, 7 Divinity Ave, Cambridge,
AA 02138
Tel: 617-495-1812
Fax: 617-495-8557
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Other_ESTs: id94q04.yl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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qi08hil.xl Soares_NhHMPu_SI Homo sapiens cDNA clone IMAGE:1855941
3' similar to contains Alu repetitive element,, PENA sequence.
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1984/05.yl Human insulinoma Homo Sapiens ethA FOT no IMAGETS644585
57. MENA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: mixed (see below); Vector: FT7T3D-Pac
Charmacial with a modified polylinker: Site_1: Not I:
Site_2: Eco RI: Equal amounts of plasmid DNA from tiree
normalized libraries (melanocyte 2NbHM, fromtant uterus
NbHDU, and fetal hear: NbHHT9W) were mixed, and ss circles
were made in vitro. Following RAP publication, this DNA
was used as tracer in a subtractive hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reaction. The driver was PCR-amplified conAs from pools of 5000 clones made from the same 3 libraries. The pocis consisted of I. M.A.G. E. Clones 250242 265224, 340488-345479, and 484488-489479.
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Melton, D., Brown, Kenty, G., Permutt, A., Lee, C., Kaesther, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwok, I., Ciliten, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, L., Blistain, A.,
                                                                                                                                                                                                   Homo sapiens
Bukaryota, Metazoa, Chordata, Cianiata, Vertebrata, Euteleostomi,
Mammalia: Eutheria, Primates, Catarrhini: Hominidae: Homo.
1 (bases 1 to 391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Pooled human meiacocy;e. :v:a; heart. and pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                   NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Freject (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLN: : contact the
IMAGE Consortium (infolimage.llnl.gov) for further information.
Insert Length: 1507 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:1855941"
/clone_lib="Soares_NHHMFu_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AAAB1408 414 bp mRNA linear EST 14-AUG-1997 2v02g09.sl NCI_CGAP_GCB1 Homo sapiens CDNA clone IMAGE:746368 3' similar to contains Alu repetitive element; mRNA sequence. AAAB1408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University protocol (http://genome.wustl.edu/est/lambda_protocol.shtmi).
Please contact Hiroshi Inoue, WD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, WO 63110). Note: this is a Washington University Pancreas EST project library.

**A Washington University Pancreas EST project library.**
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Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Organism-"Homo sapiens"
/db_xref-"taxon:9606"
/db_xref-"taxon:9606"
/clone=lih-Human insulinoma"
/Lissuc_type-"lnsulinoma"
/lab_host="DH10B (phage-resistant)"
/note-"corgan: pancreas; vector: pBBluescript SK-; Site_1:
/hois-"corgan: Constructed with lambda ZAPI! system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
                                                                                                                                                                                                Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                             Email: dmeltor@biotp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: GapBbs-ramail.nlh.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.S., Gerald Marti, M.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.

CONA Library Arrayed by: Greg Lennon, Ph.D.
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                                                                                                                                                                      Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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                                                                                                                                      Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                          Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                       Fax: 617-495-8557
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Alb/1942 MCI_CGAP_Gas4 Homo sapiens CDNA clone IMAGE:2255773 3/
Similar to contains Alu repetitive element; contains element TARI
repetitive element; mkNA sequence.
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www.bio.lbf.gov/Dbrp/image/image.html
Insert Length: 1074 Std Error: 0.30
Seq primer: -400P from Glovo
High quality sequence stop: 400.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution; information can be
found through the I.M.A.G.E. Consortium/LLNC at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Pharmacia), digested with Not 1 and closed into the Not 1 and Eco RI sites of the modified p1773 vector, library
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O
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Fh.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Lite Technologies, Inc.
CDNA Library Arrayed by: Greq Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
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Eukaryota, Metazoa, Chordata, Srabiata, Vertebiata, Euteleostomi,
Mammalia, Eutheria, Primates, Catairhini, Hominidie, Homo,
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Double-stranded CDNA was ligated to Eco RI adaptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo." 112 \varepsilon=86~q=110~t
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100.0%; Pred. No. 4.40-09;
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/do_xref-"cols:5945900"
/db_xref-"taxon:9606"
/clone="IMAGE:746368"
/clone=lib="NGT_CGAR_GCB1"
/tissue_type="germinal center B cell"
/lab_host="bH108"
                                                                      www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -41ml3 fwd. ET from Amersham
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                                                                                                                      High quality sequence stop: 400.
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Anote—Vector: PITT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eo RI; Plasmid DNA from the normalized library NcI_GAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization of 5,000 clones made from the same library (cloneIDs 1557096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Hento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A1337065 417 bp mRNA linear EST 15-FEB-1999 gx82q11.xi NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2009060 3' similar to contains Alu repetitive element; mRNA sequence. A1337065
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                                         /clone_lib="NCL_CGAP_GGS4"
/clone_lib="NCL_CGAP_GGS4"
/tissuc_type="poorly differentiated adenocarcinoma with
signet ring cell features.
/lab_host="UHiOB"
/lab_host="Cloned" Vector: pCMV-SPORT6, Site_1: Sall;
Site_2: Not!: Cloned unidirectionally. Primer: 01:49 dT.
Average insert size 1.69 kb. Life Technologies catalog #:
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Eukaryota: Metazou; Chordata; Craniata: Vertebrata: Euteleostomi;
Bammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 417)
NCI-CGAP http://www.ncbi.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
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1.8%; Score 52; DB 9; Lv
Best Local Similarity 100.0%; Pred. No. 4.3e-09;
Matches 52; Conservative 0; Mismatches 0;
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Insert Length: 528 Std Error: 0.00
Seq primer: -400P from Gibco
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/organism-"Homo sapiens"/db_xref-"taxon:9606"
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Email: cgapbs-remail.n.h.gov

Tissue Procurement: Christopher Moskaiuk, M.D., F.E.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Lite Treamologies, 15.0.

CDNA Library Arrayed by: Greg Lemmon, Ph.D.

CDNA Library Arrayed by: Greg Lemmon, Ph.D.

Clone distribution: NCl-CGAE cloue distribution ..formation: can be found through the 1.M.A.G.E. Consortium/ELNL at:

Www.blo.lhh.gov/bbrp/image/image/image.html

Seg primer: -400P from Gibco
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/db_xref="taxon:9606"
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similar_to_contains_Alu_repetitive_clement;, mkNA_sequence
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Anote "Organ: uterus_tumor; Vector: pucl8, Site_1: Smal;

Anote "Organ: uterus_tumor; Vector: pucl8, Site_1: Smal;

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derived from ORESTES PCR (U.S. Letters Patient application

No. 196.716 - Ludwig Institute for Gancer Research)

No. 196.716 - Ludwig Institute for Gancer Research)

Profiles into the pucl B vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.

a 122 c 97 g 120 t
Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Losses 1 to 450)

Dias Neto.E., Garreia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nadai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunsitein, A., deoliveire, P.S., Bucher, P., Jongeneel, C.V., ("Hare M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwigo.org.br/scripts/gethtml2.pl?tl-IL3&t2-IL3.UT0117-160301-502-G10&t3-2001-03.1&t4-1)
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP interfee Institute, Cancer Genome Anatomy Project (CGAP), Thmor Gene Index Unpublished (1997)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Emaii: cgapbs-rimail.nih.gov
This clone is available royalty-free through LLNL ; contact the
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                                                                                                                                                                                                                                                                                                                                                           Proc. Nati. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2004)
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100.0%; Pred. No. 4.1e-09;
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/db_xref="taxon:9606"
/clone_lib="CT0117"
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Location/Qualifiers
1...450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A1089524.1 GI:3428583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Conservative
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Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and closed into the Not I and Eco RI sites of the modified p1773 vector. Library continuation one round of normalization, and was constructed by Bento Soares and M. Fatisa Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           861 NCC-50 LS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: pSPORT1; Site_1: Sall: Site_2: Not1: KNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty free through LLN: contact the IMAGE Consortium (infodimage.lnl.gov) for further information. Seq primer: 40ml3 fwd. ET from Amersham High quality sequence stop: 448.
IMAGE Consortium (info@image.llnl.gov) for furthar information.
Insert Length: 761 - Std Error: 0.60
Seg-primer: -40ml3 fwd. ET from Amersham
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                                                                                                                                     /clone="IMAGE:1676040"
/clone_lib="Soarcs_total_retus_Nb2HF8.9#"
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/db_xref-"taxon:9606"
                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                 High quality sequence stop: 444.
Location/Qualifiers
                                                                                                                                                                        /dev_stage="8-9 weeks"
/lab_host="DH108"
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Contact: Wilson RK
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Fax: 314 286 1810
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493 bp mRNA linear EST 26-MAR-2002 UI-H-E10-ayh k-22-0-UI.Sl NCL_CGAP_E10 Homo Sapiens cDNA clone HAGE:5838861 3', mRNA sequence. BQ007739 BQ007739 EST CEST.
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/ db_xref-"taxon:9606"
/ clone-lib" No.1: GAP_ELO*
/ tissue_type-"Chondrosarcoma"
/ dv_stage_"Adult."
/ db_host-"OHlob (Life Technologies)*
/ note-"Ordan: Lett Polvis; Vector: pT7T3-Pac (Pharmacia)
/ note-"Ordan: Lett Polvis; Vector: pT7T3-Pac (Pharmacia)
/ note-"Ordan: Lett Polvis; Note-"Ordanis de polylinker; Site-I: EcoR I: Site-2: Not I:
/ NO.1: GAP_ELO is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
was prepared from a pool of 6 anonymous Wilms' tumor RNAs. FNA was prepared by acid-phenol, followed by one round of oligo dr selection. CDNA library preparation was with the BRULLife Tech. Superscript Plasmid system. An oligo-dr Not1 primer for first strand synthesis generated agrocerce(t) at the 3' end of the clones. A 5' Sall adaptor was used with sequence 5'-grogaccacycgroga? Resulting cDNAs were size selected (average size 2 kb), Not1 dispested, and ligated into Not1/Sall-cut pspokt1. Library was constructed by Dr. Manfred Gessier.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cqqpbs:fmail.nbi.gov
    Tissue Procurement: Dr. Jose Mercuende
    CubA Library preparation: Dr. M. Bento Soares, University of Iowa
    CubA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
    DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
    Clone Distribution: Clone distribution information can be round
    through the I.M.A.G.E. Consortium/LDML at: http://image.ilnl.gov
    The following repetitive elements were found in this cDNA
    sequence: 310-440, >ALU
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute. Cancer Genome Anatomy Project (GGAP),
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100.0%; Pred. No. 3.9e-09;
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Matches 52; Conservative 0; Mismatches
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RPCF-11-230P5.TV RPCF-11 Homo Sapiens genomic close RPCF-1:-230P5,
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Clones are derived from the human BAT library RETTIL. For BAT
Clones are derived from the human BAT library availability, please contact Ereter de line
(pieter?dejong med.bb/falo.argain.line). These better de line
BATPAC Resources (http://barpar.med.bdlfalo.adu/.ider.nia) or from
Research Genet cs (intofressen nime). BAT entile rearth pages:
http://www.tigr.org/tdb/humapen/human.nia.search/han.end.search.html.
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Mammalia: Eutheria: Primates: Catarchini: Homo.com: Homo.
1... (bases 1 to 501)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of BAC End Sequences from Library RP(1-1) for Sequence Ready
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/mote="Vector: pRAN'e3.6: Site_1: BroRI: Site_2: BroKI:
RPCIII Human Male BA' Library"
s 123 c 167 a 165 t
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J.C.
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                                                                                                                                                                                               Length 4330
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Other GSSs: RPCI-11-249P5.TJ
Other GSSs: RPCI-11-249P5.TJ
Ochtart: Shaying Jano, William Nierman. Mark Adams
Department of Enkaryotic Genomics
The Institute for Genomic Research
7712 Medical Center Dr., Rockville, MD 25850
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                            DB 14; 1.
3.9e-69;
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Rest Local Similarity 100.0%; Pred. No. 4.8e 09;
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100.0%; Pred. No. ...
1... 0; Mismatches
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/db_xref="GD8:7588;uU"
/db_xref="taxon:9606"
/clone="RPCI-11-280P;"
/cione_llb="RPCI-1;"
/sex="Male"
TAG_LIB=UI-H-E10
TAG_TISSUE=chondrosarcoma
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AQ489571
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 530)
Hedge.Pu. Oi.R.; Abernathy.K.; Dharap.S.; Gaspard.R.; Gay.C.; Holt
1.E.; Saeed.A.I.; Sharov.V.; Lee,N.H.; Yeatman,T.J. and
Quackenbush.J.
                              EST383813 MAGE resequences, MAGL Homo sapiens cDNA, mRNA sequence.
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Enkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Jases 1 to 845)
Mahalias;G.O., Wallare.J.C., Smith,K., Swartzell,S., Holzman,I.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. ar
                                                                                                                                                                                                                                                                                                                                                                            Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray
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Clones are derived from the human BAC library RPCI-II. For BAC
Library, avaitability, please contact Preter de Jong
(Fieler-decentaimed buffals, eds). Clones may be purchased from
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Proc. Nati. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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linear
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Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockwille, MD 20850, USA
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//bc.xref-"taxon:9506"
/clone_lib-"MAGE resequences, MAGL"
/note-"Vector: pBluescriptsKm"
a 139 c 111 g 145 t
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High Throughput Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: johnqatigr.org
Plate: 294
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Fax: (20%) 616-3887
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Matches 52; Conservative
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Fax: 301 838 0208
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S NCI-CGAP http://www.ncbi.nlm.mib.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.mib.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.mib.gov/ncicgap.
Lundr Gene Index.
Lundr Gene Is available toyally: tec throan Lunk a contact: the IMAGE Consortium (info@image:llmi.may) ter turther intormation.
Insert Length: 470 Std Error 6.00
Seq primer: -40ml3 fwd. El from Areisham.
High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: EroPI; Site_2: Ecoki; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EroKI and EroRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EroKI sites" 6 others
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(Pharmacia) with a modified polyfiner: Site_1: Not I:
Site_2: ECO RI: Equal amounts of posmic tend Iron
Discourse in the second of the second of the program of the
normalized libraries; because yet whree mixed, and ss circles
Were made in vitto. Following May publication, this tona
was used as tracer in a subtractive hybridization
reaction. The driver was PCM septimed or MAS for public
5,000 clones made from the same fitheries. The posts of
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BACPAC Resources (http://bacpac.med.buffalo.edu/ :derina_bac.htm) or from Resear h Genetics (into@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 895 row: E column: 20
Seq primer: 17
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Mammalia, Eutheria, Primates, Cutarrhini, Hominioae, Homo.
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/clone-lib-"Scares_NhimMou_S1"
//issue_type-"Pooled human melanocyte, :rtal heart, and
pregnant uterus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scaps
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Best Local Similarity 100.0%; Pred, No. 3.6e-09;
Matches 52; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          /clone="Plate-895 Col-20 ROW-E"
                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
                                                                                                                                                             High quality sequence stop: 545.
Location/Qualifiers
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AV718287 FHIR Home Sapiens cluna clone FHTBABHO2 5', mRNA sequence. AV718287 LGCCT-2000 AV718287 LGCCT-2000 ENTERNOR SEQUENCE. AV718287 LGCCT-0815439 EST.
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Venter,J.C.
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                                                                                                                                                                                                                                                                                                     AQ589333 71-50 DNA linear GSS 07-JUN-1999
CITBL-EL-2645K6.TF CITBL-EL Homo sapiens genomic clone 2645K6, DNA
sequence.
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Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M14-21
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="sperm"
/note="Vector: pBeloBACll; Site_1: EcoRl; Site_2: EcoRl;
                                                                                                                                            Gaps
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consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.* I others
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                                                                                                     Length 583;
                                                                                                                                                                           464 CTCACTGTAACCTCTGCCGGGTTCAAGCGATTCTCCTGAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
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                                                                                               / Match 1.8%; Score 52; DB 9; Le Local Similarity 100.0%; Pred. No. 3.5e-09; nes 52; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.1e-09;
tive 0; Mismatches 0;
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Exar: 301 8/8 0208
Email: hbe@tigr.org
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/clone="2645K6"
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Best Local Similarity 100.0
Matches 52; Conservative
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                                                                                                  Xiao,H., Peng,Y., Song,H., Gu,Y., Yana,Y., Gac,S., Xu,X., Li,N., 
Olan,B., Liu,F., Qu,J., Gao,X., Clenq,Z., Xu,Z., Stug,E., Xu,S., Gr
.W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhonq,M., Lt.; . Chon,Z., and Han
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Eukaryote McLazoa, Chordata, Craniatar Verrebbari, Enteleostudi;
Eukaryote McLazoa, Chordata, Cranifici, Hominiator Homo.
1 (bases 1 to 17)
Adams M.D., Rounsley, S.D., Zhao, S., Hass, S., Linter, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Con, ... and Venter, J.C.
Use of human BAC End Sequences to: Sequence Penely Map Huilding
Onpublished (1998)
                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebratu, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Eccinidae, Homo.
1. (bases 1 to 753)
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                                                                                                                                                                                                    Umpublished (2000)
Contact: Zequang Han
Chinese National Homan Genome Center at Shandtar.
351 Guo Shoujing Road, Zhangjiang Hi Tech Park, Teshay, Shandhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clones are derived from the human BAC library SPOI-11. For EAC
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                              Email: hanzq%chqc.sh.cn
This clone is available at CHGC in Shanshai.
Location/Qualifiers
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3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type-"hypothalamus"
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/db_xref="taxon:9656"
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100.0%; Pred. No.
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/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone-"FHTBABHC2"
                                                                                                                                                                                                                                                                                  201203, P. K. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="FHTB"
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Haliler,L. Allen,M., Howles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,M., Wylie,Y., Wylie,T., Waterston,R. Steptoe,M., Tan,F., Theising,B., Washie,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA562976 Linear EST 12 NOV-199 ac52bUl.sl Stratagene fetal retina 937202 Homo sapiens CDNA clone IMAGE:865185 3' similar to contains Alu repetitive exement: mRNA
                                                                                                                                               /cell_type="Lymphocytes"
/note "Vector: pHACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIl} Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This close is available royally-free through LLNL; contact the IMAGE Consortium (info@imade.llnl.gov) for further isformation. Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 216.
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Contact: Wilson RK
Washingto: University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63168
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/db_xref-"taxon:9606"
/clone-"IMAGE:866185"
/clone_lib_"Stratagene fetal retina 937202"
                                                                                                                                                                                                                                                                                      Length 171.
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100.0%; Pred. No. 1.8e-08
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1. 171
Acganism-"Homo sapiens"
Ab_xref-"toRe:7522510"
Ab_xref-"taxon:9606"
Acione-"RPD1-11-59J23"
Accome-"RPD1-11-59J23"
Asx-"Male"
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Fax: 314 286 1810
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BF924753/c
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                                                                                                              H90008 360 bp mRNA linear ESI 28-NoV-1995 yu83404:s1 Soares fetal liver sphenn lNFLS Homo sipiens cbnA clone LMAGE:240389 3' similar to contains Alu repetitive element; contains MERZE, repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                              EST 06-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE Consortium (info@image.llnl.gov) for sursher intormation. Insert Length: 1095 Std Error: 0.00 Seq primer: Promega -21ml3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, M. 13108
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:3789442"
/db_xref="Laxon:9606"
/clone=!iMAGE:240389"
/clone_lib="Soares fetal liver spiren lNETS"
Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="20 week-post condeption tetus"
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This clone is available royalty-tree through LLNI.
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100.0%; Pred. No. 1.1e-08
tive 0; Mismatches 0.
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High quality sequence stops: 320
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
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Matches 51; Conserv
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DRIGIN
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890008/c
Locus
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BF924753 375 bp mRNA linear EST 19-JAN-2001 CM1-WF0209-281100-609-C10 NT0209 Homo sapiens CDNA, mRNA sequence. HF924753
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                                                                                                                                                                                                                                    1 (bases 1 to 369)
Hillier.L. Allen,M., Bowles.L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
J., Moorc,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,J., Waterston,R. and Wilson,R.
                                                                                                                                                       Homo sapiens
Eukaryota: Metazoa: Chordata; Cranlata: Vertebrata; Euteleostomi;
Manmalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
MAGE:841103 5' similar to contains Alu repetitive element;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 2381 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: cst@watson.wustl.edu
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/db_xref="taxon:9606"
/clone="IMAGE:841103"
/clone_lib="Stratagene lung (#937210)"
/sex-"male"
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100.0%; Pred. No. 1.1e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
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High quality sequence stop: 361.
Location/Qualifiers
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                                                            AA486970.1 GI:2217134
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Theres 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
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BAC ends
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A0178114
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                                                                                                                                                                                                                                                                                                                                           AQ280600 379 bp that Theorem GSS 22-NeV 1998 CITHLED-2516H22.TR CITHLED Saptems of nomine clone 2516H22.
                                                                                                                                    Fax: -55-11-2707001
Email: asimpson@ludwig.org.bt
Email: asimpson@ludwig.org.bt
Phis sequence was derived trom the FAPESP/LICR Burn. Cancer Genome
Project. This entry can be seen in the tol.cwing TRL
(http://www.ludwig.org.br/scripts/qethtml2.pl?!: :MIs12-cM1-NT0209-281100-609-c108t3-2000-11-286t4*1)
Seq primer: pur B forward
High quality sequence stop: 374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are available from Research Genetics (into resquencem), BAC
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Adams, M.D., Rounsley, S.D., Zhao, S., Bassis, Liniari, K., Goldanik, Berry, K., Granger, D., Suh, E., Wiblect, Shicuyare, Simon, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/harrend_search.htm..
Seg primer: M13 Reverse
                                                 Laboratory of Cancer Genetics
Ladwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 acdar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496
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Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.8%; Score 51; DB 12; I
ilarity 160.0%; Pred. Nc. 1.1e-08;
Conservative 0; Mismatches 0;
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Other GSSs: CITBI-E1-2516H22.FF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                  Contact: Simpson A.J.G.
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                                                                                                                     Tel: +55-11-2704922
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                                                                                                        Brazil
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                                                                                                                                                                          /note-"Vector: pBeloBACI1; Site_1: EcoRI; Site_2: EcoRI; CalTech Human BAC Library D"
98 c 111 q 85 t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams.M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism~"Homo sapiens"
/db_xref-"taxon:9606"
/clone="Plate=2217 Col=2 Row=L"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109,
TEL: (206) 616-3618
Fax: (206) 626-3887
Email: )wallace@u.washington.edu
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100.0%; Pred. No. 1.1e-08;
tive 0; Mismatches 0;
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00.0%; Pred. No. 1.1e-08;
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                                       /ordanism-"Homo sapiens/
/db xet-"taxon:9606"
/clone-"2516H22'
/clone-11b-"CITBI-EI'
/sex-"male'
/cell_type-"sperm'
/note-"Vector: pbeloBACII;
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Homo sapiens
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/fab_nost="Publish (ampleilln resistat)
/fab_nost="Organ: liver and spleen vector: gi7180 (Pharmacia)
with a modified polylibrater; Site_i: Par i Site_2: Fro R::
fst strand cDNA was pinned with a fact = 0.1mo(d) gitiger
// Actograph and polylibrater; Site_i: Par i Site_2: Fro R::
fst stranded cDNA was pinned with Par i and site of the dapters
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and Eco RI sites of the modified pinned with laboury
went through one round of notralization. Library
                                                                     yr20d65.81 Soares fetal liver spleen INFLS Homo syriets cDNA clone
IMAGE:205833 3' similar to contains Alu repetitiva element: Ontains
THR repetitive element; mRNA sequence.
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Eukaryota, Metazoa: Chordata: Craniata; Verlebia:: Euteleostomi;
Eukaryota, Metazoa: Chordata: Craniata; Verlebia:: Euteleostomi;
L. (bascs L. to 448)
Hilliari, Clark, N., Dubuque, T., Elliston, K., Harxins, M., Holman, M., Hullman, M., Kodaba, T., Lehm., Lennon, G., Karia, M., Parsons, J., R., Williamson, A., Wohldmann, P. and Wilson, R., Waterston The Washu-Warck ESI Project
Contact: Wilson RK
Contact: Wilson RK
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RPCI-11-280612.TJ RPCI-11 Homo sapiens genomic class RPCI-11-280612
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131 c = 103 g = 114 t = 2 others
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Fax: 314 286 1810
Fax: 314 286 1810
Finali: est@eatson.wustl.edu
High guality sequence stops: 353
Source: IMAGE Consortium, LLNL
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/db_xref="GDB:3774964"
/db_xref="taxon:9606"
/db_cref="taxon:9608"
/clone="IMAGE:205833"
/clone=lib="Soarcs fetal liver spleen lNFLS"
/sex="male"
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Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ (bases 1 to 479)] [ Mahairas G.G. Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                   Email: hbe#ligr.org
Clones are derived from the human BAC library RPCI-:11. For BAC
Library availability, please contact Pieter de Jong
(pieter?dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
thtp://www.ligr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: SP6
Class: BAC ends.
   Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Rominidae: Homo.
                                                                                       Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                           Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
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AQ334511 G1:4129372
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                                                                                                                                                                                                 Unpublished (1997)
Contact: Shaying 2hao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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9.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 1.8%; Score 51; DB Local Similarity 100.0%; Pred. No. 9.4 nes 51; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                            The Institute for Genomic Research
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Eukaryota, Metazoa,
Mammalia, Eutheria,
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RPCI11-113P19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11 113P19,
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Eukaryota, Metazoa, Chordata, Craniata, Verrebratar Eureleostomi,
Mammalia, Eutheria, Primates, Catarihini, Hominidas, Homo.
                 Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (...to&resgen.rom).
AbC and Web Server: http://www.htsc.washington.ed.
Plate: 587 row: 1 column: i5
Seq primer: T?
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jord,P. and Venter
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Other_GSSs: RPC111-113P19.TV
Contect: Shaying Zhao, William Nietran. Ma
Contect: Shaying Zhao, William Nietran. Ma
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, Mp 206
Fax: 301 838 0200
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9.4e-09;
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100.0%; Pred. No.
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Fax: (206) 616-3887
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Contact: Kobert Strausberg, Ph.D.

Email: cyapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., D.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., Ph.D., DNA Sequencing by: Greg Lennon, Ph.D., DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Not-CGAP clone distribution information on through the 1.M.A.G.E. Consortium/LLNL at:

Www-bio.llni.gov/bbrp/image/image.html
Www-bio.llni.gov/bbrp/image.html
Washing.sequence stop: 415.
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531 bp mRNA linear EST 16.0EC-1999
4220903.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE:2289101 3'
51milar to contains Alu repetitive element;contains L1.t3 L1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryolu; Metazoa; Chordata; Craniata; Vertebrata; Euteleoslomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 531)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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adenocarcinoma, 3 pooled tumors"
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Conservative 0; Mismatches 0;
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Email: bbeeligr org
Clones are available from Research Genetics (informesgen.com). BAC
end search page:
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Seg primer: MIR Reverse
class: BAC ends.
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Calrech Human BAC Library 5"
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/clone_lib-"CITBI-EI"
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1. .539
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Search completed: May 10, 2003, 01:55:16 Job time : 4476:15 secs

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